

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw mode!

Run on: April 13, 2006, 12:51:03 ; Search time 189 Seconds

(without alignment)
683.478 Million cell updates/sec

Title: US-10-686-490D-2

Perfect score: 1 MAQVKANGITLLEYEEQGHHRH.....ERHIFRLIELIAGHAAAAAA 294

Sequence: Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43337871 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqP19808;*: 2: geneseqP19908;*: 3: geneseqP20008;*: 4: geneseqP20016;*: 5: geneseqP20028;*: 6: geneseqP200348;*: 7: geneseqP200348;*: 8: geneseqP20048;*: 9: geneseqP20058;*: 10: 227.5 15.1 271 7 ADI23937 6 ABU21130 Protein e

11: 220.5 14.6 276 6 ABU21130 Protein e

12: 216.5 14.3 264 7 ADI23904

13: 209.5 13.9 259 4 AAG64664 Hydroxyn

14: 209.5 13.9 259 8 ADOT0988

15: 204 13.5 271 9 AA022154 Ramoplatin

16: 203.5 13.5 264 9 AEB39939 L. pneumo

17: 201.5 13.5 280 9 AEB36545 L. pneumo

18: 198 13.1 232 7 AAE24160 Human alp

19: 198 13.1 232 8 ADT05828

20: 198 13.1 232 8 ADT05777

21: 198 13.1 232 8 AAR10975 Polyydro

22: 196 13.0 283 2 ABO73720 Pseudomon

23: 192 12.7 287 7 AAB60302 Alpha/bet

24: 189.5 12.6 251 4 AAB60302

ALIGNMENTS

RESULT 1
ADO26338 ID ADO26338 standard; protein: 294 AA.

XX AC ADO26338;

XX DT 29-JUL-2004 (first entry)

XX DE Anti-Kazlauskas lipase protein.

XX KW ds; gene; enzyme; anti-Kazlauskas lipase; esterification; hydrolysis; pharmaceutical; agricultural chemical; liquid crystal compound.

XX OS Synthetic.

XX PN EP1418237-A2.

XX PD 12-MAY-2004.

XX PF 06-OCT-2003; 2003EP-00022590.
XX PR 16-OCT-2002; 2002DE-01048166.

XX (PARB) BAYER CHEM AG.
XX PA Bosch B, Meissner R, Barendes F, Koch R;
XX PI DR WPI; 2004-378759/36.
XX DR N-PSDB; AD026337.

XX PT New nucleic acid encoding anti-Kazlauskas lipase and derived enzymes, useful for stereospecific hydrolysis and synthesis of aralkyl esters, intermediates for pharmaceuticals and plant protection agents.

XX Claim 11; Page 16-17; 22pp; German.

CC The present invention provides the protein and coding sequences of an anti-Kazlauskas lipase. These are used as catalysts in esterification or hydrolysis reactions for preparation of enantiomeric aralkanols, or their esters, useful for preparing pharmaceuticals or agricultural chemicals, also liquid crystal compounds. The present sequence is the protein of the invention.

SQ Sequence 294 AA;

Query Match 100.0%; Best Local Similarity 100.0%; Pred. No. 1e-151; Length 294;

Matches	294;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	Best Local Similarity	46.9%;	Pred.	No. 1.4e-55;
Qy	1	MAQVANGTTLVEYEQHRHPSMMLINGGGOLIDWPEEPTRGLAERGRVVICFNDNDA	60							Matches 134;	Conservative 49;	Mismatches	98;
Qy	1	MAQVANGTTLVEYEQHRHPSMMLINGGGOLIDWPEEPTRGLAERGRVVICFNDNDA	60							Qy	7 NGITLEYEBQCHRHHPSMMLINGGGOLIDWPEEPTRGLAERGRVVICFNDNDA	TKL	66
Db										Db	33 NGILHEVEVGKPKENETILLIMGLGAQMFLWPDEFFCKSLIDQGPVIRPDRNDIGSSKV	92	
Qy	61	GISTKLEGVKCNPNTARVFLASNLGKPVPPYTDMDTVGLMDALGIESTHVGVSMG	120							Qy	67 -EGYTKPNTPARVFLASNLGKPVPPYTDMDTVGLMDALGIESTHVGVSMG	123	
Db	61	GISTKLEGVKCNPNTARVFLASNLGKPVPPYTDMDTVGLMDALGIESTHVGVSMG	120							Db	93 RHQG-KRLNTMKGFLPALGRNQGAPTYLDMADDVSMLLDRLGUSKAHYIGASHGGM	151	
Qy	121	GMAAQILGAKHGERVKSLLMTISSGNPRMPAPRQVTKFVRPKSMDKEEINTKYNLEL	180							Qy	124 AQILGAKHGERVKSLLMTISSGNPRMPAPRQVTKFVRPKSMDKEEINTKYNLEL	183	
Db	121	GMAAQILGAKHGERVKSLLMTISSGNPRMPAPRQVTKFVRPKSMDKEEINTKYNLEL	180							Db	152 AQILAKYPERKEVLGMLFTSNNNPQLPPFPKQNLICKPESRDEBEGTVNHSJMLFQL	211	
Qy	181	LTTTGSPIDRECLADLYRKTSIERTCLCEGTQDQLAAILQSRSRVKLLRRIAVPTLVISG	240							Qy	184 IGSPG-LDREKLALDVRKSSTERCLCEGTQDQLAAILQSRSRVKLLRRIAVPTLVISG	242	
Db	181	LTTTGSPIDRECLADLYRKTSIERTCLCEGTQDQLAAILQSRSRVKLLRRIAVPTLVISG	240							Db	212 IGSPG-TINHLEAVQTPARKLYQRTSYPPAGVLTQQFLALLCCTSLLQDRETKPLVHGSR	271	
Qy	241	AEDPLPYQCGRDIAHDHPGARFELIGMGHDPERHPRLIELIGHAAEEA	294							Qy	243 DPLLPYQCGRDIAHDHPGARFELIGMGHDPERHPRLIELIGHAAEEA	288	
Db	241	AEDPLPYQCGRDIAHDHPGARFELIGMGHDPERHPRLIELIGHAAEEA	294							Db	272 DRLLPSHKGKAVAKAISGAKFELIDGMGHDIPAHFTPQLSGLFAHK	317	
<hr/>													
RESULT 3													
ID	ADR51257	standard; protein:	299 AA.							ID	ADR51257	standard; protein:	299 AA.
XX										XX			
AC	ADR51257;									AC			
XX										XX			
DT	04-NOV-2004	(first entry)								DT	04-NOV-2004	(first entry)	
XX										XX			
DB	Anti-biofilm polypeptide #24.									DB			
XX										XX			
KW	antibacterial; antiinflammatory; anti-biofilm polypeptide;									KW			
KW	humoral response; environmental sample; water; liquid; soil; air;									KW			
KW	biological sample; medical device; pharmaceutical; food product;									KW			
KW	cosmetic; hygiene product; water treatment device; water transport; pulp;									KW			
KW	paper processing; paper recycling equipment; toothpaste; chewing gum;									KW			
KW	mouthwash; dental cleaner; caries; plaque; gingivitis; periodontitis;									KW			
KW	oropharyngeal colonization; gastric colonization; thermostability;									KW			
KW	thermotolerance.									XX			
OS	Unidentified.									OS			
XX										XX			
FH	Location/Qualifiers									FH			
FT	Key									FT			
FT	Domain									FT			
FT	49 . 288									FT			
/note= "alpha/beta hydrolase fold domain"													
PA	WO2004066945-A2.									PA			
XX										XX			
PD	12-AUG-2004.									PD			
XX										XX			
PR	2004W0-US00242.									PR			
XX										XX			
PR	26-JAN-2004;									PR			
XX										XX			
PR	24-JAN-2003;									PR			
XX										XX			
PA	DIVERSA CORP.									PA			
XX										XX			
PN	W02004066945-A2.									PN			
XX										XX			
PD	12-AUG-2004.									PD			
XX										XX			
PR	2004W0-US00242.									PR			
XX										XX			
PR	26-JAN-2004;									PR			
XX										XX			
PR	24-JAN-2003;									PR			
XX										XX			
PA	DIVERSA CORP.									PA			
XX										XX			
PI	Barton N, Robertson D, Chang K, Elkins J;									PI			
XX										XX			
WPI	2004-625102/60.									WPI			
DR	N-PSBB; ADR5156.									DR			
XX										XX			
PR	New anti-biofilm enzymes such as esterase, glycosidase, amylase, useful									PR			
PT	for controlling biofilms on a wide range of household, industrial,									PT			
CC	medical surfaces ^s .									CC			
CC	Claim 45; SEQ ID NO 48; 413pp; English.									CC			
CC	The invention relates to an isolated or recombinant anti-biofilm									CC			
SQ	Sequence 322 AA;									CC			
Query Match	40.3%; Score 607.5; DB 6; Length 322;									CC			

sequence identities is determined by analysis with a sequence comparison algorithm or by visual inspection. (I) is useful for making an antibody by administering to a non-human animal (I) or a DNA (II) encoding (I), to generate a humoral response. Oligonucleotide primers (III) are useful for isolating or recovering (II) encoding (I) from an environmental sample comprising water, liquid, soil, air or biological sample derived from a bacterial, protozoan, insect, yeast, plant, fungal or mammalian cell. (I) is useful for making a small molecule by providing several biosynthetic (I) capable of synthesizing or modifying a small molecule, and reacting the substrate with enzymes. (I) is useful for preventing the growth of a biofilm on a medical device, pharmaceutical, food product, device for making a food, cosmetic, hygiene product, water treatment device, water transport or storage device or pulp and paper processing and paper recycling equipment. The pharmaceutical (I) is a tablet, pill, implant, suppository, inhaler, spray or ointment. The biofilm is from Pseudomonas or *Staphylococcus*, which involves administering to the biofilm (I) having esterase activity. (I) is useful in cleaning and decontaminating hard surfaces such as floors, equipment, machinery and industrial water treatments. (I) is useful as preservatives in food, medicinal, hygiene, and cosmetic products, useful in toothpaste, chewing gum, mouthwashers, dental cleaners. (I) is useful for controlling dental biofilms associated with caries, plaque, gingivitis, and periodontitis. (I) is useful for treating oropharyngeal and gastric colonization by pathogenic microorganisms. The activity of (I) is thermostable or thermotolerant. This sequence corresponds to a polypeptide of the invention.

Sequence 299 AA;

Query Match 39.6%; Score 597; DB 8; Length 299;

Best Local Similarity 45.1%; Pred. No. 1.7e-54; Matches 128; Conservative 43; Mismatches 111; Indels 2; Gaps 1;

Db 8 IIELEYEQQHRHPSMILIMGLCGQOLIDWPEPIRGIAERGSRVICPDNRDAGLSTKLEG 68

Db 8 TIEYEYETGHPDPAIVLIMGLGGQLTIPVREDNRDGLSTLDH 67

Qy 69 VCKPNIARFVSMGLKPRPVPTLDDMADTVGLMDALGTESTHVVGSNGCMIAQILG 128

Db 68 LPRPNPLPLAALRQLRLPVRASITLDDMADDVAGLLDANIKQAHVVGSNGCMIAQIL 127

Qy 129 AKHGERYKSLTIMITSSGNPRMPAPRQPKMVRPKMSDKBEWIKYNELLETTIGSPG 188

Db 128 ARHATRVTSRSLTIMITSSGARVNPQGSPGQMRMENMIRRDTSRBGLIRHGMRTWRIIGSP 187

Qy 189 LDREKLALD--VRKSISRCILCPGTOPOLAATLQSRSRKVLRRIAVPTLVSGAEDPLI 246

Db 188 YPKPEAHLTRIVAEQFDRAFHAGEMOLHAAAPSAPLPRKOPADYTHGDLLV 247

Qy 247 PYOCGRDIADH1PFGARFLIEGMHD1PERH1PRLIBAGHA 290

Db 248 PYAAARDLVRRLPENATLDPVGMGHDPTEIMPRIARRIVETAA 291

Qy 243 DPLLPYQCGRDIAHDH1PFGARFLIEGMHD1PERH1PRLIBAGH 288

Db 273 DRLLPDSHGKAVAKATGAKFELIQMGHD1PPHPTPQLSYLFHH 318

RESULT 5

ABB09185

standard; protein; 321 AA.

XX AC ABB09186;

XX DT 04-JUL-2002 (first entry)

XX DE Acinetobacter calcoaceticus carboxyl esterase #2.

XX KW Pseudomonas aeruginosa; esterase; estA; enzyme; enantiomeric;

XX KW optical active carboxylic acid; asymmetric hydrolysis; hypertension;

XX KW carboxylic ester racemate; hypertension; analapril; captoril.

XX OS WO200132847-A1.

XX PD 10-MAY-2001.

XX XX

PF 01-NOV-2000; 2000WO-KR001243.

XX PR 01-NOV-1999; 99KR-00047927.

XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
PA (BIOTH-) BIOHOLDINGS INC.

XX PI Kim C, Rhee S, Song K, Lee J, Boyapaty G;

XX XX DR WPI; 2001-316432/33.

XX PT Novel esterase derived from *Pseudomonas aeruginosa* useful for producing

PT optical active carboxylic acids and pharmaceuticals, preferably

PT hypertension treatments drugs like analapril or captoril.

XX PS Example 6; Fig 3; 40pp; English.

XX The present invention describes an esterase (I) derived from *Pseudomonas aeruginosa* which has a sequence comprising 315 amino acids, and produces optical active carboxylic acids and enantiomeric isomers by the asymmetric hydrolysis of the carboxylic ester racemates. (I) has hypotensive activity. (I) is useful for producing optical active (R)-carboxylic acids, preferably optical active (R)-carboxylic acids from carboxylic acid ester racemates. (I) is useful for the production of various kinds of physiologically active pharmaceuticals, especially hypertension treatments drugs like analapril or captoril. (I) has excellent ability for producing optically active carboxylic acids from carboxylic acid esters. Production of optically active carboxylic acids by (I) is highly more selective, simple and environmentally favorable when compared to conventional techniques. (I) is thermally stable at high temperatures above 70 degrees Celsius. The present sequence represents a carboxyl esterase amino acid sequence given in comparison with the esterase of the present invention.

XX SQ Sequence 321 AA;

XX Matches 130; Conservative 53; Mismatches 100; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 321 AA;

XX Query Match 39.1%; Score 589.5; DB 4;

XX Best Local Similarity 45.5%; Pred. No. 1.2e-33;

XX Matches 33; Mismatches 53; Indels 3; Gaps 3;

XX Sequence 3

KW carboxylic ester racemate; hypertension; analapril; captoril.
 XX Acinetobacter calcoaceticus.
 XX WO200133847-A1.
 XX 10-MAY-2001.
 XX 01-NOV-2000; 2000WO-KR001243.
 XX PR 01-NOV-1999; 99KR-00047927.
 XX (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 PA (BIOH-) BIOHOLDINGS INC.
 XX P1 Kim C., Rhee S., Song K., Lee J., Boyapaty G.;
 XX DR; 2001-316432/33.
 XX Novel esterase derived from *Pseudomonas aeruginosa* useful for producing
 PT optical active carboxylic acids and pharmaceuticals, preferably
 PT hypertension treatments drugs like analapril or captoril.
 XX PS Example 6: Fig 3; 40pp; English.
 XX The present invention describes an esterase (I) derived from *Pseudomonas aeruginosa* which has a sequence comprising 315 amino acids, and produces optical active carboxylic acids and enantiomeric isomers by the asymmetric hydrolysis of carboxylic ester racemates. (I) has hypotensive activity. (I) is useful for producing optical active carboxylic acids, preferably optical active (R)-carboxylic acids from carboxylic acid ester racemates. (I) is useful for the production of various kinds of physiologically active pharmaceuticals, especially hypertension treatments drugs like analapril or captoril. (I) has excellent ability for producing optically active carboxylic acids from carboxylic acid esters. Production of optically active carboxylic acids by (I) is highly more selective, simple and environmentally favourable when compared to conventional techniques. (I) is thermally stable at high temperatures above 70 degrees Celsius. The present sequence represents a carboxyl esterase amino acid sequence given in comparison with the esterase of the present invention.

Sequence 312 AA;
 SQ Query Match 38.9%; Score 586.5; DB 4; Length 312;
 Best Local Similarity 45.1%; Pred. No. 2.3e-53;
 Matches 129; Conservative 54; Mismatches 100; Indels 3; Gaps 3;

Db 6 ANGITLEYEQGRHRPHPSMILINGGGQIDWPPEFIRGLAERGFVICEDNRDAGLS 65

Db 24 SNGELHVYGVGPNDHPHTILLGLAQALFWDFPFCSSLIDGFFYTRFDRDIGLSSK 83

Qy 66 LEGV-KKPNARYELLASNLGL-KPRVPYTLDDMDALTVGLDALGEESTAVYGVSMGMI 123

Db 84 IRHKGKRNLNTKLMSRTFTLGNQGAPYLYMAEDVSLLEAMRIKKVNIVGASNGMI 143

Qy 124 AOTLGAKIGERVSLSLMTTSNPRMPAPRPOVQLKMRPKSMDKEWIKYNLELLTT 183

Db 144 AQIAAKTFEKFVKELMTSANOPLLPPFPKPLGPKSSDEGGIINHSLKFEI 203

Qy 184 IGSPLGLDRKLAD-VRKSIERCLCPECTOROLAATLGSRSYKLLRIAVPTLVISGAE 242

Db 204 IGSQGYNNYEAOTARRYQSRSTYHAGVLUQQFAILCTGSUQLDQKQISQPTLVHGSR 263

Qy 243 DPLIYQQCDIADHIPSARFELLEGMDHIDPERHIFPLIELIAGH 288

Db 264 DRJLPPSHCKAVAKAIKGAKFELQJGMGHDIPIQSYLFPAHH 309

RESULT 6

AB073253 standard; protein; 422 AA.

ID AB073253

XX

AC AC073253;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #5428.
 XX KW Bacterial infection; *Pseudomonas aeruginosa* infection; antibacterial.
 XX OS *Pseudomonas aeruginosa*.
 XX PN US6551795-B1.
 XX PD 22-APR-2003.
 XX PP 18-FEB-1999; 99US-00252991.
 XX PR 18-FEB-1998; 98US-0074788P.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR; 2003-615309/58.
 XX DR N-PSDB; ABD06824.

PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

PT Disclosure; SEQ ID NO 21999; 455pp; English.

XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using bichip technology. Sequences AB067326-AB084396 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 422 AA;

Qy Query Match 37.3%; Score 562.5; DB 7; Length 422;

Best Local Similarity 43.1%; Pred. No. 1.3e-50; Mismatches 117; Indels 3; Gaps 2;

Matches 125; Conservative 45; Mismatches 117; Indels 3; Gaps 2;

Qy 4 VKANGTILEYEQGRHRPHPSMILINGGGQIDWPPEFIRGLAERGFVICEDNRDAGLS 63

Db 125 VELGDYRLAYDSIGRNSDPAUJLVMGIGGGLKPRVYLPVSAUCEQGRVIRTDNRDGLS 184

Qy 64 TKLEGKPNIARVFLLASNLGLKPRVYLPVYTLDDMDALTVGLDALGEESTAVYGVSMGMI 123

Db 185 AWNPVPPSSRLTYEVRYRLGLPVSAVPTLTDAGBLHLLDLD1PQAHVLGASMGMI 244

Qy 124 AQILGAKIGERVSLSLMTTSNPRMPAPRPOVQLKMRPKSMDKEWIKYNLELLTT 183

Db 245 AQHIAAMAPQRLLSLDLMVMTSGAGLIPAPSESLLILAR REAASREQAEQVQADLLAA 303

Qy 184 IGSPGL--DREKLALDVRSKTSERCLCPEGTORQALILOSGSRVRLKLRRIAVPTLYISGA 241

Db 304 LGSPGLYQCGRDIAHDHIPGARFELLEGMDHIDPERHIFPLIELIAGH 291

Qy 242 EDPLIYQQCDIADHIPSARFELLEGMDHIDPERHIFPLIELIAGHAAA 291

Db	364 ADPLLPVMIHGVAHRSSELKLIPLGLAHRFQEAKPEPDLAAVVPPYLKA	413	ID AAW30522 standard; protein; 267 AA.
RESULT 7			
ADL05923	ADL05923 standard; protein; 360 AA.		
XX		XX	XX
AC		AC	DT 17-OCT-2003 (revised)
AC		XX	DT 26-OCT-1998 (first entry)
XX	Kurthia sp. bioH gene-encoded polypeptide.	XX	DE
XX	Biotin; vitamin; bioH gene; pinely CoA.	XX	XX
XX	Kurthia sp. 538-KA26; (DSM 10609).	OS	KW
XX		XX	KW
XX	Moraxella catarrhalis; infection.	XX	EP853127-A2.
XX	Moraxella catarrhalis.	XX	PN
OS		XX	15-JUL-1998.
XX	US6673940-B1.	XX	XX
PN		PF	18-SEP-1997;
PR		PR	27-SEP-1996;
PD		XX	96EP-00115540.
XX	06-JAN-2004.	XX	
PF	04-APR-2000; 2000US-00540236.	PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX		XX	
PR	08-APR-1999; 99US-0158416P.	PI	Furuichi Y, Hoshino T, Kimura H, Kiyasu T, Nagahashi Y;
XX		XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.	DR	WPI; 1998-364652/32.
XX		DR	N-PSDB; AAV42058.
PI	Bretton GL;	XX	
XX	WPI; 2004-178127/17.	PT	New DNA and vectors encoding polypeptides - used for recombinant
DR		PT	production of biotin.
XX	N-PSDB; ADL04003.	XX	
PT	PT	PS	Claim 1; Page 24-25; 45pp; English.
PT	PT	XX	This is a polypeptide encoded by a newly isolated bioH gene (see CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is CC thought to be involved in the synthesis of the biotin precursor pimelyl CC COA. Polypeptides (see AAV4 18-25) encoded by novel bioH, bioA, bioP, CC bioB, bioII, bioHII and bioC genes (see AAV4 2054-61) of Kurthia CC sp. are provided, as well as vectors comprising one or more of the genes, CC transformed cells, and a process for the production of biotin that CC comprises cultivating the transformed cells and isolating biotin from the CC culture medium. Biotin is used in the preparation of pharmaceutical, food CC or feed compositions. The synthesis is an improvement on prior CC methods involving fermentation of e.g. E. coli and <i>Bacillus sphaericus</i> , CC which have low productivity due to accumulation of DB, a biocin CC precursor. (Updated on 17-OCT-2003 to standardise OS field)
XX		XX	
SQ	Sequence 360 AA;	Sequence 267 AA;	
Query	32.0%; Score 481; DB 8; Length 360;	Query Match 20.8%; Score 314.5; DB 2;	
Best Local Similarity 37.3%; Pred. No. 3.1e-42;	Best Local Similarity 33.1%; Pred. No. 1.8e-24;	Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;	
Matches 107; Conservative 61; Mismatches 111; Indels 6; Gaps 3;	Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;		
QY	8 GITDYEBCGHRHPSMLIIMGQLIWPBPPIRLERGFRVICPDRNDRGSLTK--	QY	1 MAQVKANGITLVEEBOGRHHPSMLIIMGQLIWPBPPIRLERGFRVICPDRNDRGSLTK--
Db	42 GIKLVEAGGNPERPPMTTGLGSQMMWPSDQFLKRPFDAGPFIIRDNRDTGLSSKIQ	Db	1 MPFVNHDNESELYVE--HGQGDPLLIMLGQTNLSW-HRTVTFLAKR-FKVTFDNGV
QY	66 LEGYKPNIARVPLASMGKPR--VPTLDMDALDTGLMDALGIESTHYGVSMGM 122	QY	121 GMIAQILGAHKGERVKSPLTMITSQNSNPMPAPRQV--LQKFMRVPKSMDKEWVW---
Db	102 IDGIPRLNTPRMKLUKMQAGLUSNRBSPVATLTDNAEDARLKLTMQLNVNLLGASMGM 161	QY	61 GISTKLEGVKPKNIAVFLASMGKPR--VPTLDMDALDTGLMDALGIESTHYGVSMGM 120
QY	123 IAQILGAHKGERVKSPLTMITSQNSNPMPAPRQV--LQKFMRVPKSMDKEWVW-	Db	57 GKSS-----KEQPYSTEMMAEDARAVLDAVSVDARYVGISMG 95
Db	162 IAQIQAARYPKYIQLVLFSTNSRAFLPFPNPQFMTVRPPEHSERDVMRHSVWFM	QY	121 GMIAQILGAHKGERVKSPLTMITSQNSNPMPAPRQV--LQKFMRVPKSMDKEWVW-
QY	183 TIGSPG-LREKCALDVRSKIERCLCPETQRQLAALSRSVKKRRIAVPTLVSGA 241	Db	96 GMIAQILGAHKGERVKSPLTMITSQNSNPMPAPRQV--LQKFMRVPKSMDKEWVW-
Db	222 AVGSPGHLDIKGTRAIACERYQRMNPHPLXVSQQTALLASRSIRFTQIRANTLVHGN 281	QY	174 IKYNLELITIGTSPGLOREKLAQVRSKIERCLCPETORQLAAILQGSRVKLLRRIAV
QY	242 EDPLPQYQCRDIAHDHPARFELTEGMCHDIPERHPIPLIELJAGH 288	Db	223 IYVSQAFIEK--HPELQO---DQKRQEITTPSAYLSQLOQACTLHTDSNS-LDKINI 208
Db	282 KGDLIVAPNGKILLKAXVISARFLVLDGMHDLPNTYYPPLNLISEH 328	QY	234 PTIVISGAEPLPQYQCRDIAHDHPARFELTEGMCHDIPERHPIPLIELJAGH 271
Db		Db	209 PHLIHGDADNLVPPENGKMLAERIQQSOFHTVSCAGH 246
RESULT 8			
AAW30522			

RESULT 11

Db	192 LSA--ADDORGEDLAGITAPCRVIAFADDIVAPPHLAKBIADALPEADWVHPDCGHYGY 248
Qy	272 -DITERHPIRLI 282
Db	249 LERPDR-VNRLI 259

ABU21130 standard; protein; 276 AA.

ID ABU21130;

XX DT 19-JUN-2003. (first entry)

DB Protein encoded by Prokaryotic essential gene #6657.

XX Antisense: prokaryotic essential gene; cell proliferation; drug design.

KW Burkholderia fungorum.

OS

XX WO200271183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00348992.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0342699P.

XX PA (ELIIT-) ELIITA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseni KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,

XX DR WPI: 2003-028926/02.

XX DR N-PSDB; ACA25000.

PS Claim 25; SEQ ID NO 49054; 176pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*, CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of CC the target prokaryotic essential genes. Note: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX

Sequence 276 AA;

Qy	3 QVKANGTILEYREOGHRHRHPSMILIGGQLDIPPEEFIRGLAERGERFVICIDNRDAGL 62
Db	8 EITVRGOTISYNBLGDBR-TULLLHGHTSDASINWLST-MPALAQRSWRVIAFDQLGFGQ 65
Qy	63 STYLEGVKPKPNTRAVFLASMGCLKPRVPTYLDDMALDTVGILMDALGLESTHYVGNSMGM 122
Db	66 SS-----KPSV-----PVRPRTLSDM-----VAPUDALGLEMVSIVGQSNCGH 104
Qy	123 IAGILGAXRHGEVKSTLIMITSQG-NPRMPAPR-----PQVLOKEMRVPKSMDFE-- 171
Db	105 VAGLPAQOYPVEREAVLVNVAGYGLAPEVDPRDLGHAVTPGGL-WALNPATRDSSR 162
Qy	172 -EWIKYNNLELTITGSPGLDRBKLAUDVRKSIECLCPEGTOROLAAILOGSRR----- 224
Db	163 LIEMVFIDQGLVTEELIDGFYADRLG-----KGIGAVRISISESWARREDTL 209
Qy	225 ---VKLLRRIAVPTLVISGAEDPLLPYQGRDIAHDHPGARFELLGGMGDIP 274
Db	210 ESAFTGLERR---PVNVIQARQDKVAYHGLGRAHEGIAERSRFVVLSDCGHAPP 260

RESULT 12

AD123904	ID AD123904 standard; protein; 264 AA.
XX	AC AD123904;
XX	DT 22-APR-2004 (first entry)

DE Streptomyces fradiae A541 locus ORF8 protein.

XX antimicrobial; fungicide; viricide; gene therapy; lipopeptide synthesis;

KW KW A54145; NRRL 3143; antimicrobial; antifungal; antiviral;

XX KW A541 biosynthetic locus; ORF8.

OS Streptomyces fradiae.

XX US2003198981-A1.

PN

XX 23-OCT-2003.

PD

XX 24-DEC-2002; 2002US-00323079.

PF

XX 26-DEC-2001; 2001US-0342133P.

PR

XX PR 17-APR-2002; 2002US-1372789P.

PR

XX PR 03-SEP-2002; 2002US-00232370.

XX

PA (ECOPIA BIOSCIENCES INC.

XX Parnet CM, Staffa A, Zazopoulos E;

XX WPI: 2003-852704/79.

DR N-PSDB; AD123905.

XX

PT New isolated, purified or enriched nucleic acid, useful for synthesizing PT Lipopeptides, particularly from the biosynthetic locus A54145 and NRRL PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.

XX

PS Claim 10; SEQ ID NO 18; 69pp; English.

The invention describes an isolated, purified or enriched nucleic acid (I) comprising: any of 4 fully defined regions: a nucleic acid having at least 75% sequence identity to a nucleic acid of (a) or complements of (a) or (b). The methods and compositions of the present invention are useful for synthesising lipopeptides, particularly A5415 and NRRL 3143, exhibiting antimicrobial, antifungal or antiviral activity. This is the amino acid sequence of the protein encoded by *Streptomyces fradiae* A541 biosynthetic locus ORF8.

XX Sequence 264 AA;

Query Match	14.3%	Score 216.5; DB 7; Length 264;
Best Local Similarity	25.8%	Pred. No. 5e-14;
Matches	79;	Conservative
	44;	Mismatches 104; Indels 79; Gaps 10;
Qy	5	KANGTLEYEKGHRHHPSPMLIMGLGGIDWPEFGLAERGFRVCFDNRDAGLST 64
Db	4	RINGDLDHERRG--SGSPSLLNGSGAATGWLHQDALVAAGFEAWTFTR----- 55
Qy	65	KLEGYKKPNTARVELLASHMGLKPR--VPYTLDDMADLTGILMDALGIESTHYVG 121
Db	56	-----GTPSGCGPPTQDMAADTIGLIBHLGJGCAVGTGSIKA 96
Qy	122	MAIQILGAKHGERVKSLTMITMSGNPRMPA-----PRPOVLOQEMKR- 163
Db	97	RVACEVARYARPDLYSRCVNMAPRARAADRTRAATAAEI ALADSGVTVPRYAVRAMON 156
Qy	164	-VPKSMDKEWIKNLEL-LTTIGSPGLDREKLALDVRSKIERCLCPGTORQLAAILQ 220
Db	157	LSPTPLADDERIAWDLDFELAAAGPG-----ARTOLEISAVYH 196
Qy	221	SGSRVYKLRLRIAVPTLVISGQAEDPLPYQCGRDIADHTPGARFELIEGMGH---DIPER 276
Db	197	--REEDLARITAPCRVIAFADDIVAPAHLAKEIADALPEADYHVVPDCGHGYLEQDFR 253
Qy	277	HIPRLI 282
Db	254	: -VNRLI 258

RESULT 14

ADO70988 standard; protein; 259 AA.

XX ID AAG64664

XX AC AAG64664 standard; protein; 259 AA.

XX DT 14-SEP-2001 (first entry)

XX DE Hydroxyindol-related protein #9.

XX Xanthomonas maltophilia; 7-hydroxyindol; 7-hydroxytryptophan; drug;

XX dyestuff; reagent.

XX OS Stenotrophomonas maltophilia.

XX PN JP2001095577-A.

XX PD 10-APR-2001.

XX PR 28-SEP-1999; 99JP-00273961.

XX PR 28-SEP-1999; 99JP-00273961.

XX (SAOC) MERCIAN CORP.

XX DR WPI; 2004-299744/28.

XX PA N-PSDB; ADO70979.

XX PT Preparing sesamol, useful as raw material for pharmaceuticals, comprises carrying out biotransformation of 1,3-benzodioxole.

XX PS Disclosure; Page; 25pp; Japanese.

XX CC New Xanthomonas maltophilia DNA sequence, useful in a method for producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw materials for drugs, dyestuffs and reagents.

CC Disclosure; Page 17-18; 23pp; Japanese.

CC This invention relates to a *Stenotrophomonas maltophilia* (Xanthomonas maltophilia) DNA sequence which encodes 9 proteins. The invention includes a method for the production of 7-hydroxyindol and 7-hydroxytryptophan in which a micro carrying a fragment of the DNA sequence is capable of hydroxylating the 7-position of indol is cultured. The DNA is useful in a method for producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw materials for drugs, dyestuffs and reagents. The present sequence represents a protein encoded by the DNA of the invention

XX SQ Sequence 259 AA;

Query Match

14.3%; Score 216.5; DB 7; Length 264;

Best Local Similarity

25.8%; Pred. No. 5e-14;

Matches

79; Conservative

44; Mismatches 104; Indels 79; Gaps 10;

Qy 5 KANGTLEYEKGHRHHPSPMLIMGLGGIDWPEFGLAERGFRVCFDNRDAGLST 64

Db 4 RINGDLDHERRG--SGSPSLLNGSGAATGWLHQDALVAAGFEAWTFTR----- 55

Qy 65 KLEGYKKPNTARVELLASHMGLKPR--VPYTLDDMADLTGILMDALGIESTHYVG 121

Db 56 -----GTPSGCGPPTQDMAADTIGLIBHLGJGCAVGTGSIKA 96

Qy 122 MAIQILGAKHGERVKSLTMITMSGNPRMPA-----PRPOVLOQEMKR- 163

Db 97 RVACEVARYARPDLYSRCVNMAPRARAADRTRAATAAEI ALADSGVTVPRYAVRAMON 156

Qy 164 -VPKSMDKEWIKNLEL-LTTIGSPGLDREKLALDVRSKIERCLCPGTORQLAAILQ 220

Db 157 LSPTPLADDERIAWDLDFELAAAGPG-----ARTOLEISAVYH 196

Qy 221 SGSRVYKLRLRIAVPTLVISGQAEDPLPYQCGRDIADHTPGARFELIEGMGH---DIPER 276

Db 197 --REEDLARITAPCRVIAFADDIVAPAHLAKEIADALPEADYHVVPDCGHGYLEQDFR 253

Qy 277 HIPRLI 282

Db 254 -VNRLI 258

RESULT 14

ADO70988 standard; protein; 259 AA.

XX ID ADO70988;

XX AC ADO70988;

XX DT 15-JUL-2004 (first entry)

XX DE Stenotrophomonas maltophilia sesamol production-related protein #9.

XX XX sesamol preparation; 1,3-benzodioxole; pharmaceutical preparation;

XX KW antihyperpertensive; sesamol production-related gene cluster.

XX OS Stenotrophomonas maltophilia.

XX PN JP2004105064-A.

XX PD 08-APR-2004.

XX PR 18-SEP-2002; 2002JP-00271076.

XX PR 18-SEP-2002; 2002JP-00271076.

XX PA (SAOC) MERCIAN CORP.

XX DR WPI; 2004-299744/28.

XX PT Preparing sesamol, useful as raw material for pharmaceuticals, comprises carrying out biotransformation of 1,3-benzodioxole.

XX PS Disclosure; Page; 25pp; Japanese.

XX CC The invention comprises a method for preparing sesamol, the method involves using a strain of *Stenotrophomonas maltophilia* to convert 1,3-

CC benzodioxole to sesamol. The Stenotrophomonas maltophilia bacteria
 CC contains a gene cluster (9320 nucleotide sequence given in the
 CC specification) that is involved in the conversion of 1,3-benzodioxole to
 CC sesamol. The method of the invention is useful for preparing sesamol
 CC which can be used as a synthetic raw material for pharmaceuticals such as
 CC antihypertensives. The present amino acid sequence represents a protein
 CC encoded by the Stenotrophomonas maltophilia sesamol production-related
 CC gene cluster of the invention.

XX Sequence 259 AA;

Query Match 13.9%; Score 209.5; DB 8; Length 259;

Best Local Similarity 28.9%; Pred. No. 2.7e-13; Mismatches 36; Indels 57; Gaps 10; Matches 82; Conservative 36; Mismatches 109; Indels 57; Gaps 10;

Qy 4 VKANGITLVEEQGRHHSMSMLIIMGCGCILW-----PPEFIRLAEGCFRVCIFD 56

Db 13 VVANGIRTNTHDAG--DGAPVLMHGSGGVSAWANWLTMPB----LATR-FRVIAFD 64

Qy 57 NRDGGLSTLEGVKKPKNLARVPELLASMGLKPRVPTYLDMDALGIBESTHVVG 116

Db 65 MVGRGYQSOPPEGIH-----YSLDTWNQAVALLDIEQASVVG 104

Qy 117 VSMGGMIAQIGLGAQHGERVSLTIMITSGNPMPNPAQPVQOKFMRVPKSMDKEEMIKY 176

Db 105 NSFGAIALLAALATRHPRKVRLVLM---GSVGVSFPTBGLDAVWGYQPSVBS----- 153

Qy 177 NLENLTTTCSPGIDREKLADLWRKSIEFLCPGTQRLAAIL---QSG-----SRVKL 227

Db 154 NMRLDIFRA--YDRKLVNDELAQMRYKASIOPQFBFSAMFPAPQNGMMAPIEQ 211

Qy 228 LRRTAIVPTIVISQGAEDPLPYQGRDIADHIFGARFELJEGMGH 271

Db 212 IRGIEHOTLIVVHGREDKYTPLQNSYELLQAIQNAQLHVFGKCGH 255

SQ Sequence 271 AA;

Query Match 13.5%; Score 204; DB 5; Length 271;

Best Local Similarity 25.0%; Pred. No. 1.e-12; Mismatches 38; Indels 76; Gaps 9; Matches 78; Conservative 38; Mismatches 120; Indels 76; Gaps 9;

Qy 4 VRANGITLVEEQGRHHSMSMLIIMGCGCILW-----PPEFIRLAEGCFRVCIFD 63

Db 9 VTINGPRLAYRSAGEB--PVLMIMGSAGOTWTYHOTPALHEAGSSTVVEDSR----- 61

Qy 64 TKLEGTKCPNTLARVFLLASMGLKPRVPTYLDMDALGIBESTHVVGSMGMI 123

Db 62 -----GPBSDV-----PAGYSLADMADTRGLBALDIAPCRIVGTSLSAMI 105

Qy 124 AQLGAKHGERVKSLLIMITSSGNPPRMPAPRQ----VLQKEMRVPKSMDK----- 170

Db 106 AQELAVDHPPELVRCVALIATLARPDDARAQNOADLLESQTVLPAYEATAVFRMFS 165

Db 171 -----EWIKVNLELLTIGSGLDREKLADLWRKSIEFLCPGTQRLAAILQ 220

Db 166 PATLNDDVAVREWLDI-FELSGTGVSAG-----GQAVAEI- 199

Qy 221 SGSRVXLLRRAVPTLVISGAEIDLPLPYOCGRDIAHDIPGARFELJEGMGH---DIPER 276

Db 200 TGDRRALRSATPCRVISFADDLTFPHLLAEVAAPCDOLVEISRCGHGLGYLERPDA 259

Qy 277 HIPRLIELIGH 288

Db 260 VNAAILEFLDSH 271

(ECOP-) ECOPPA BIOSCIENCES INC.

XX Farnet CM, Zazopoulos E, Staffa A;

XX XX WPI; 2002-435445/46.

DR N-PSDB; AAL40781.

XX Novel isolated ramoplanin biosynthetic pathway polypeptide useful for

PT chemically modifying biological molecule that is a substrate for a

PT polypeptide encoded by a ramoplanin biosynthesis gene cluster.

Search completed: April 13, 2006, 12:55:20
 Job time : 192 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using sw model

Run on: April 13, 2006, 12:55:38 ; Search time 41 Seconds

Title: US-10-686-490D-2
Perfect score: 1509
Sequence: MAQVKANGITLVEEGHRH.....ERHPRLLIELIAGHAAAAAA 294Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : PIR_80;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	589.5	589.5	39.1	321	1	SS7530	carboxyl esterase
2	562.5	562.5	37.3	328	2	D83197	probable hydrolase
3	498	498	32.1	301	2	C70614	probable ligG prot
4	475.5	475.5	31.5	304	2	B71446	probable hydrolase
5	327.5	327.5	21.7	298	2	D71339	trans protein - Str
6	312.5	312.5	20.7	282	2	D9552	probable hydrolase
7	268.5	268.5	17.8	272	2	T36181	probable hydrolase
8	268.5	268.5	17.8	459	2	I60717	streptothricin-ace
9	234.5	234.5	15.5	265	2	A1G313	probable hydrolase
10	229.5	229.5	15.2	268	2	C96028	probable 3'-oxoadip
11	228.5	228.5	15.1	262	2	E70548	probable bpoC prot
12	227.5	227.5	15.1	276	2	T30594	conserved hydrolase
13	217.5	217.5	14.4	261	2	T35708	hydrolase - Strept
14	211.5	211.5	14.0	256	2	A1G313	chloride peroxidase
15	211	211	14.0	262	2	S34609	carboxylesterase (
16	210	210	13.9	300	2	AG3214	cultivar specifici
17	200.5	200.5	13.3	393	2	B87548	hypothetical prote
18	196.5	196.5	13.0	238	2	A69463	2-hydroxy-6-oxo-6-
19	196	196	13.0	283	2	B3B604	poly (3-hydroxyalka
20	195	195	12.9	258	2	AB2770	hydrolyase (impore
21	195	195	12.9	261	2	C97550	hydrolyase (AJ27164
22	192	192	12.7	265	2	F83586	probable hydrolase
23	187	187	12.4	265	2	AB3115	beta-ketoacidate e
24	187	187	12.4	265	2	C98172	beta-ketoacidate e
25	186.5	186.5	12.4	275	2	F83243	probable hydrolase
26	184.5	184.5	12.2	647	2	C96834	unknown protein F5
27	182	182	12.1	263	2	C83616	beta-ketoacidate e
28	182	182	12.1	614	2	E9658	unknown protein, 1
29	180	180	11.9	285	2	S29306	poly (3-hydroxyalka

RESULT 1		
SS7530		
carboxyl esterase - Acinetobacter calcoaceticus		
C:Species: Acinetobacter calcoaceticus		
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		
C:Accession: SS7530		
R:Rok, R.G.; Barr, A.; Hellingwerf, K.J.		
submitted to the EMBL Data Library, June 1995		
A:Description: Characterization of the estBR operon of Acinetobacter calcoaceticus BD4.		
A:Accession: SS7530		
A:Status: preliminary		
A:Molecule type: DNA		
A:Residues: 1-321 <ROK>		
A:Cross-references: UNIPROT:Q57172; UNIPARC:UPI00001727AA; EMBL:X66895		
A:Start codon: GTG		
C:Superfamily: carboxyl esterase		
Query Match Similarity 39.1%; Score 589.5; DB 1; Length 321;		
Best Local Similarity 45.5%; Pred. No. 1.5e-41; Mismatches 53; Indels 100; Gaps 3;		
Matches 130; Conservative 53; Gaps 3;		
Query 6 ANGITLEYEQGHRHHPSMILLIMGLGQLIDPPEPIRGLABRGFVTCDFNDAGIYSTK 65		
Db 33 SNGLELHVVEGVGNPDHTTILIMGLGQMLFWPDFFCKSLIDQGFYVIRFDNRDIGHSSK 92		
Query 66 LBGV-KCPNIAEVFLASMGML-KPRPYTLDMDALGIESTHVVGSIGM 123		
Db 93 IRHKGRRLNTKLMSRTLGLGNQGAPYLIDMAEDVSILLEAMRKVNVIGASIGMM 152		
Query 124 AQILGAKHGERVKSLSMITTSGGNPRMPAPRQVOLKFMRPKSMDEKEWIKYNLELLTT 163		
Db 153 AQAIAKYPEKVLALMFTSNNOPLIPPPFKOLSLIGPKSSDEGIIINISLKLPEI 212		
Query 184 ICSPGCLDREKLAID-WRKSIERCLCPRTGTQRQLAAILOGSVKYLARRIAVPTLYISGAE 242		
Db 213 IGSPGVYNQVNEAIQTARKLYQSYHPAGVQVLOOFPLATCTGSNLQLDKQISQPTLVHGSR 272		
Query 243 DPLPLPYOCGRDIADHFPGARFELJEGNGHIDPERHLPLIELIAGH 288		
Db 273 DRLLPSHKGAVAKAGAKFELIQMGHDIBPHFIPOLSYLFAH 318		

RESULT 2
D83197
probable hydrolase PA3586 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004

C:Accession: D83197

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Li, adman, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li;

A; Molecule type: DNA
 A; Residues: 1-298 <UR>
 A; Cross-references: UNIPROT:054528; UNIPARC:UPI00000B37D6; GB:UJ0405; NID:9505668; PIDN:
 C; Superfamily: carboxyl esterase

Query Match Score 21.7%; DB 2; Length 298;
 Best Local Similarity 29.9%; Pred. No. 9.1e-20;
 - Matches 97; Conservative 41; Mismatches 119; Indels 67; Gaps 10;

Qy 4 VKANGTLEYEEOGRHPPMLLIMGLGGOLIDPEEFERGLAERGFRVTCFONDRAGIS 63
 Db 6 VPSGDVEILNSDDFGDPADPAILLIMGNNSALGPDEPARRLADGGLHYTRYDHDRGRS 65

Qy 64 TKELEGVKPNIARYELLASMLKLDRPVPTLDDMALTHYDGLMDALGIESTHVYGVSMGAM 123
 Db 66 T-----TRDFAAH-----PYGFGEELIADAVAVLDGNGVDRKAVVLSMGATI 107

Qy 124 AQILGAKRGERVSKSLTLM-----TSSGNPRMPA PRPQVLOKEM----- 162
 Db 108 TQVIALDHDRLSSTTMGGGLDIDPDANIERTMRGETLDPGPQ-QPPLDALALM 165

Qy 163 -----RVPKSNDEKEWIKYNLELLTTIGSFLDRLKALDVRSKIERCLCPEG----- 210
 Db 166 NPQAEGRAAEVARVSK-W----RILSGTGVFPDDAYARNE----ERADHAGCVL 213

Qy 211 --TQRQLAIIQLGSRSRVKLLRRIAVPTVYVSGABDPLPYQCCRDIAHDTPGARFELIEG 268
 Db 214 AEPAHYSTLTPPSRASABRETVPTVYVQAEHDPIAFAPGRKHLADLIPTARLAEIPEG 273

Qy 269 MGHDIPERHPIRLEIAGHAAA 292
 Db 274 MGHALPSSVHGPLAEVILAHTRSA 297

RESULT 6

D9352 probable hydrolase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
 C; Species: Sinorhizobium meliloti
 C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C; Accession: D9352
 R; Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowes, J.; Kalman, S.; Kasting, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98: 9883-9885, 2001
 A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti genome. Reference number: A95262; PMID:11396509; PMID:11481432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-282 <UR>
 A; Cross-references: UNIPROT:092YY8; UNIPARC:UPI00000CBLA8; GB:AE006469; PIDN:AAK65382.1;
 A; Experimental source: Strain 1021, megaplasmid pSymA
 R; Galibert, P.; Finan, T.M.; Long, S.R.; Phueller, A.; Abola, P.; Barloy-Hubler, F.; Bowes, J.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, L.; Hyman, R.W.; Jones, T.
 Science 293: 668-672, 2001
 A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Klop, C.; Lelauré, heubault, P.; Vandembol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A; Reference number: A96039; PMID:21369234; PMID:11474104
 A; Contents: annotation
 C; Genetics:
 A; Gene: SMa127
 A; Genome: Plasmid
 C; Superfamily: carboxyl esterase

Query Match Score 20.7%; DB 2; Length 282;
 Best Local Similarity 31.3%; Pred. No. 1.5e-18;
 - Matches 93; Conservative 39; Mismatches 128; Indels 37; Gaps 7;

RESULT 6

Qy 61 GLSTKLEGVKPKNIARYELLASMLKLDRPVPTLDDMALTHYDGLMDALGIESTHVYGVSM 119
 Db 61 GLSTK-----YPPQGQYAFDNADAVDVRVLDGYRISAAHVGNSL 101

Qy 120 GGMIAQIILGAKRGERVSKSLTLMITS---SGNPRMPAPRQVQKFMRYPKSMDEKEWIKY 176
 Db 102 GGMIQATALKHBERVSLTAISSSPVGMNTTHLPASCTAWMDHMNMEVDWSDEAAY 161
 Qy 177 NLE-LITTPSPGLDREKLDVRSKIERCLCPEG----TQRQLAILQSRSRKVL 228
 Db 162 MLDARLYASTVHPDEAE----TRAFITERDERSCGYLSATINHSVTLIFEISDAWQDR-L 215
 Qy 229 RIAVPTLVISGAEDPLPYQCGRDIADHTPGARFELIEGMDHPERHIPRLIELI 285
 Db 216 PEKVLPLVTHGTADPPVPEVHGAAVATAVDGARLVEEGGGELHPADWDKTSAI 272

RESULT 7

T36181 probable hydrolase - Streptomyces coelicolor

C; Species: Streptomyces Coelicolor

C; Date: 03-Jun-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C; Accession: T36181
 R; Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, A; Submitted to the EMBL Data Library, March 1999
 A; Reference number: 221600
 A; Accession: T36181

A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA
 A; Residues: 1-272 <SHU>
 A; Cross-references: UNIPROT:Q9Z4Z8; UNIPARC:UP100000DAF2A; EMBL:AL035707; PIDN:CAB3887
 A; Experimental source: strain A3 (2)
 C; Genetics:

A; Gene: SC0DB; SCE29.0
 C; Superfamily: carboxyl esterase

Query Match Score 17.8%; DB 2; Length 272;
 Best Local Similarity 26.8%; Pred. No. 6.7e-15;
 Matches 85; Conservative 44; Mismatches 109; Indels 79; Gaps 10;

Qy 1 MAQYKANGTLEYEQ----GHRHPSMLLINGGOLIDWPPEFIRGLAERGFRVICRD 56
 Db 1 MPVLTNGIRINYDAPPAGQNAPOAVLLYNGGSGCRWHLHQVPLVAAGFRVISPD 60

Qy 57 NRDAGLSTKLEGVKPKNIARYELLASMLKLDRPVPTLDDMALTHYDGLMDALGIESTHVYGV 116
 Db 61 NRGTAPESECPG-----GFGIDDVLVDTAALVBERLGPCRVAG 99

Qy 117 VSMGGMIAQILGAKRGERVSKSLTLMITSSGNP-----RMPAPRQV 157
 Db 100 ISNGAHAQELALSRSPLDVDRVLMATRA-RDPALEREALCRAEMELYDGQIRLPAAYERV 158

Qy 158 LOKFMRV-PKSMDKE---EWIKYNLLELTIGSPGLDREKLDVRSKIERCLCPEGTO 212
 Db 159 VQAMQNLSSPRLNDQARDLWLDV-LELTRSGA-----GYR 194

Qy 213 ROLAALQOSRSVYKLIRRIVAPTLVYSGAEDPLPYQCGRDIADHTPGARFELIEGMDH 271
 Db 195 AOL-GVRVDGDREREATGIRAAATRVAFQDDLIAPPHLGREVADAIPGAEYELVDPDCSHY 253

Qy 272 ---DIPERHIPRLIELI 285
 Db 254 GYLESPDAVNKSIVEFL 270

RESULT 8

160717 streptorhycin-acetyl-transferase - Escherichia coli

C; Species: Escherichia coli

C; Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

R; Tieje, E.; Brevet, J.
 Plasmid 25, 217-220, 1991

Qy 1 MAQYKANGTLEYEQGHHRHPSMLLINGGOLIDWPPEFIRGLAERGFRVICRD 60
 Db 1 MLIKGNDVBIATEAFGDSAHPPVVLVQGMSMNLWWPERFCRRVAFRRVAFQDDLIAPPHLGREVADAIPGAEYELVDPDCSHY 253

A;Title: The trimethoprim resistance transposon Tn7 contains a cryptic streptothricin resistance gene A;Reference number: 160717; MUID:92021239; PMID:1656477	Db	156 LNDVAVADWIAFMNWPDKS--TPGL-----RC-----PQN 190
A;Status: preliminary; translated from GB/EMBL/DBJ	Qy	223 SRYKLRLRIVAPLVIISGAEDPLPYPQGRDIADHIGARFELIEGMGH---DIPERHI 278
A;Molecule type: DNA	Db	191 NRLPAYRSTAAPLVIGFAEDVTPPSLGREVADVLPGRLQIPDAGLGFPERPEAVN 250
A;Residues: 1-459 <RES>	Qy	279 PRLELIAQ 287
C;Cross-references: UNIPROT:Q47625; UNIPARC:UPI0000AF08C; EMBL:X56815; NID:9499063; PID: C;Superfamily: streptothricin acetyltransferase	Db	251 AAUQQFFAG 259
Query Match Score 17.8%; DB 2; Length 459; Best Local Similarity 29.6%; Pred. No. 1.3e-12; Matches 86; Conservative 56; Mismatches 108; Indels 41; Gaps 13;		RESULT 10
3 QVKANGTLEYEEOQHRHHPSSMLLNGGGOLIDMPEEFIRGLAERGFRVICFDNRDAGL 62 Db 20 KVVRRAISLTTESFGDPAHPIIIMG-AMSAVWPDEFPSQLXKMRVTRDHR-AQK 77		C96028 probable 3'-oxoadipate enol-lactonase (EC 3.1.1.24) [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti
Qy 63 STKLESVKPNIARYVLLASMGKPRVPXTLDDWALDTVGIMDALGTESTHVVGYSMCGM 122 Db 78 STSYE-----psqQAPYSSVEELA-DDVTRVDGXGLEAHLVEMSICGF 118		C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: C96028 R;Finan, T.M.; Weindner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hern. Proc. Natl. Acad. Sci. U.S.A. 98, 9839-9844, 2001 A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing en. A;Reference number: A95842; MUID:11481431
Qy 123 IAQILGKAGGERVSLTLMIT--SSGNPMPMAPPVQLOKMRVPKS-MDKEWIKY 177 Db 119 LSQLV-ALNPKVRSKLTLASERLADADPMPA-FAAILEYHQRAESLSDWSRDAAVYQ 176		A;Status: preliminary A;Molecule type: DNA A;Residues: 1-268 <KUR> A;Cross-references: UNIPROT:Q92TM0; UNIPARC:UPI00000CB8A6; GB:AL591985; PIDN:CA49891.
Qy 178 LELLTIGTSP-GLDREKLADVRKSIERCLCPETGTQRLAAIQLS--GSRVKLRR 232 Db 177 VAWRNSGTAHAHFADKINQNTAHLNFD-----TPNLTTFNHTLGGERWGRNLNT 229		A;Experimental source: strain 1001, megaplasmid pSymB R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubelle, D.; Chain, P.; Cowie, A.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.; Neuhäutl, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wong, D.H.; Wong, K.; Yeh, J.; Zeng, X.; Zhou, J.
Qy 233 VPTLVISGAEDPLPYQGRDIADHIGARFELIEGMGHIDPERHIPRLIE 283 Db 230 VPTLHGTEDPVLPYVHGLAKE-ARGSKMLTLEGTHGLHHEDWPRIQ 279		A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaur, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti A;Reference number: A960339; MUID:21368234; PMID:11474104
RESULT 9 A87193 probable hydrolase [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Accession: A87193 R;Cole, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holden, M.A.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, R.; Rutherford, K.M.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Sq		A;Contigs: annotation A;Genes: PCAP; SB20579 A;Genome: plasmid C;Superfamily: carboxyl esterase C;Keywords: carboxyl ester hydrolase
A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002	Db	Query Match Score 15.2%; DB 2; Length 268; Best Local Similarity 27.2%; Pred. No. 1.2e-11; Mismatches 95; Indels 79; Gaps 10; Matches 81; Conservative 43; Score 229.5; DB 2; Length 268;
A;Accession: A87193 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-265 <STO> A;Cross-references: UNIPROT:Q9CBB1; UNIPARC:UPI000006E55; GB:AL450380; NID:913033907; F	Qy	1 MAQYKANTITLEEQQGH-RHIPSMSLLIMGLGCQIOWPEEFIRGLAERGFRVICFDNRD 59 Db 59 HGU8-----DIG----QVPTLISGAEDPLPYVHGLAKE-ARGSKMLTLEGTHGLHHEDWPRIQ 58
C;Genetics: A;Gene: ML2269 C;Superfamily: tropinesterase	Db	60 AGJSTKLEGVKKPENIARYVLLASMGKPRVPYPTLDMDALDPTVGLMDAIGIESTHVGYSM 119 Db 59 HGU8-----DIG----QVPTLISGAEDPLPYVHGLAKE-ARGSKMLTLEGTHGLHHEDWPRIQ 58
Query Match Score 15.5%; DB 2; Length 265; Best Local Similarity 26.9%; Pred. No. 4.4e-12; Mismatches 104; Indels 81; Gaps 12;	Qy	120 GGMIAQILGAKIGERVKSLTLMITSGNPRMPPQVLOKEMRVPKSMDEKEEWKYNLE 179
Matches 83; Conservative 41; Mismatches 104; Indels 81; Gaps 12;	Db	98 GGIAQSILYGRPEPDLYRALVLSGTA-----HKIGCTVEFWDA 133
Qy 9 ITLEYEEQHRHHPSSMLLNGGGOLIDMPEEFIRGLAERGFRVICFDNRDAGLSTKLEG 68 Db 2 INLVAYDRGTGE--PVVFAGRGGRGRTOPHAFLAGYRITFDNRGIGATENTG 59		180 LLTTIGSGFLDREKLADVRKSIERCLCPETGTQRLAIIQGCSRULLR-----229
Qy 69 VPKPNIARYVLLASMGKPRVPYTLDVGLMDAIGIESTHVGVSMGMAQIQLG 128 Db 60 -----PITQTMVADTAVIESGAVPARIVGSMGFSIAQELM 97		134 RITRAEAHGI--EAVADGV--LERWFTPAFRPENLAF--TGYRANMLVRQPVPGYVGTC 186
Qy 129 AKHGERVKSLTLMITSGNPR-----MPA---PPVQLOKEMRVPKS 167		230 -----RIVAVPTLISGAEDPLPYVHGLAKE-ARGSKMLTLEGTHGLHHEDWPRIQ 274
Db 98 VARPSLVRAVLMAVRGRRLRTRQFFHAAEAFFHDGTOQPSGYNAYKVRLENUSR--K 155		187 AAIRDADFTEAAGRIVAVLVCVGDQGSTPBDLVRSTADLPGARFEVIRGAGH-IP 243
Qy 168 MDKE --- EWI-KYNLELLTTIGSPGLDREKLADVRKSIERCLCPETGTQRLAIIQG 222		RESULT 11 ET0548 C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

Page 5

Db	98	SYAQELAHPEIILDAVTLMAACG-----RSLSVQVRVL---AEGEAKLJELGTTEL	145										
Qy	181	-----LTIGSPGIDREKLA---LDVRSKSIERCLPECTQRQLAIILOSRSYKL	227										
Db	146	PPGLAAATRAMENLGPAITLADDPGFLDPLTASDWGPGRQLQISNL---DIPERHPRJIE	283										
Qy	228	LRIIAVPTLVISGAEDPLPQCGRDIAHDHPARFELJEGMHH-----											
Db	203	YRAIKVCPHVISFEHDLYAPPSSAGRELLAAIPGATHRTIPGCCSHFGYLNSPEAVNELLR	262										
Qy	284	LIAGHAAA 291											
Db	263	PLRAESAA 270											
RESULT 13													
T35708	hydrolase - Streptomyces coelicolor	C.Species: Streptomyces coelicolor	C:Accession: T35708	C:Text: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004	R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.	submitted to the EMBL Data Library, January 1998	A:Reference number: 221548	A:Accession: T35708	A>Status: preliminary; translated from GB/EMBL/DDBJ	A:Molecule type: DNA	A:Residues: 1-261 <MUR>	A:Cross-references: UNIPROT:O51172; UNIPARC:UPI00000DABAF; EMBL:AU021411; PIDN:	A:Experimental source: strain A3(2)
Qy		C:Genetics:											
Db		C:Gene: SC02DB:SC7H1:13	C:Superfamily: triosephosphate isomerase										
Qy	49	GFRVICFDNRDAGLSTKLEGV/KKPNTARVELLASMGMLKPRVPYTLDDMDALTVGLMDALG	108										
Db	50	GIRAIISYDQRDSGIT-----	88										
Qy	109	IESTHVVGVSMGGMIAQILGAKHGRVKSLTMITSGGNPRNPAPRQDVLQKFMRVPKSM	168										
Db	89	LARAHLIGTSEGGAVAQHAARRHPERVASLVLVATPSYAMCSAAIDELLE-----M	140										
Qy	169	DKEEWIYKNLELTTIGSPGLIDREKALDIDVRSIERTCLPECTQRQLAIILOSRSYK-----	226										
Db	141	SHE-----DROQAADY-----FPTPEG-----OAGQRARPA	167										
Qy	227	--LIRR-----											
Db	168	IAPVTLVISGAEDPLPQCGRDIAHDHPGA	261										
Qy	262	RFLIEGMHDI 273											
Db	228	BLCPIEGRHGI 239											
RESULT 14													
AG3343	chloride peroxidase (EC 1.11.1.10) (imported) - Brucella melitensis (strain 16M	C:Species: Brucella melitensis	C:Accession: AG3343	C:Text: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 12-Jul-2004	R:De Vecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagiwara, S.; O'Callaghan, D.	Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002	A:Title: The genome sequence of the facultative intracellular pathogen Brucella	A:Reference number: AD3252; PMID:11756688	A:Accession: AG3343	A:Status: preliminary			

A;Molecule type: DNA
 A;Residues: 1-256 <KUR>
 A;Cross-references: UNIPROT:08YHR3 ; UNIPARC:UPI0000057DC7 ; GB:AE008917 ; PIDN:ARL51914.1 ;
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME10733
 A;Map position: I
 C;Superfamily: tropinesterase
 C;Keywords: oxidoreductase

Query Match 14.0%; Score 211.5; DB 2; Length 256;
 Best Local Similarity 28.2%; Pred. No. 3.5e-10; Indels 91; Gaps 12;
 Matches 82; Conservative 27; Mismatches 91; Indels 91; Gaps 12;

Qy 7 NGITLFEEQGRHRHPSMILIMGL-GGQJIDWPSE-FTIGLAERGFRVICEDNRDAGLST 64
 Db 12 DGLRLAYRQAG--EGDPILLIHGFASSSLVNPSPGMFTLCEGYRVIAIDNRGHRGST 69
 Qy 65 KLEGIVYKPNIARVFLLLASMLKPRVPTDLMALDTVGWADAGIESTHVGYSMGMINA 124
 Db 70 KSHKAE--...-----DVTDSKMRDAAALDHEGIAKHWGYSMGARIS 110
 Qy 125 QILGAKHGERVKRSITL-----MITSSGN-----PRMPA----PRPOVLOQKFNRVP 165
 Db 111 AVLATEHSERSEVHSAVFGGGIGMVGAGKWPIGEALLMLEDPATITHPGQMRPKFADQT 170
 Qy 166 KSMDEKEWVKKNLLETTIGSPGLDREKALDVRKSISERCLCPEGTQRQAAFLQSGSSRV 225
 Db 171 RS-----DRIAAACVITSKE-LVP-----V 190
 Qy 226 KLLRIIAVPTLVISGAEDPLLPYQCGRDADHPIGARFLIEGMHDPER 276
 Db 191 AAIEPILQPVIVAVGTTDDIA--CSAQELANLIP-----NGEALDPIGR 232

RESULT 15

S34609 carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)

C;Species:

Pseudomonas sp.

A;Variety: strain KWI-56

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 12-Jul-2004

C;Accession: S34609

R;Shimada, Y.; Nagao, T.; Sugihara, A.; Iizumi, T.; Yui, T.; Nakamura, K.; Fukase, T.; I
Bichim. Biophys. Acta 1174, 79-92, 1993

A;Title: Cloning and sequence analysis of an esterase gene from Pseudomonas sp. KWI-56.

A;Reference number: S34609 ; PMID:93326640 ; PMID:8334166

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-262 <SH1>

A;Cross-references: UNIPROT:09Z1UB ; UNIPARC:UPI00000B7399 ; GB:D14529 ; NID:9397834 ; PIDN:

C;Superfamily: tropinesterase

C;Keywords: carboxylic ester hydrolase

Query Match 14.0%; Score 211; DB 2; Length 262;
 Best Local Similarity 26.4%; Pred. No. 4e-10; Indels 64; Gaps 9;
 Matches 77; Conservative 44; Mismatches 107; Indels 64; Gaps 9;

Qy 7 NG-ITLEYEEQGRHRHPSMILIMGL-GGQJIDWPSE-FTIGLAERGFRVICEDNRDAGLST 65
 Db 5 NGNVNLSDIVAGHGE--CFFIAGTAGSDKSMW--DGLRLBELSKYRTAFDNRDGSESTI 60
 Qy 66 LEGYKKPNIARVFLLLASMLKPRVPTDLMALDTVGWADAGIESTHVGYSMGMINA 125
 Db 61 CD-----OYTMNDLAKDALSYMDAEGLQKAIHGHSLGNTIAQ 99
 Qy 126 ILGAKHGERVKRSITLIMITSSGGNPMAPPQVLOKEMPKNSMDKEEKVYNLELTITG 185
 Db 100 ELLAIAPDVSITLIVNTA--RDNVMSVIELARDWSKTTDQRULNRSVYF--- 152
 Qy 186 SPGLDREKALDVRKSISERCLCPEGTQRQIAILOGSGSVKLRR----- 230
 Db 153 --ALGSKALGSDIFNQVV-----DFAQSOSQSPREALIRQWEIDLTVDTDRSL 200

Qy 231 IAVPTLVISGAEDPLLPYQCGRDIAADHPIGARFELIGMGH---DTPERHI 278
 Db 201 INAKTHVIWASEDKVTRKDQQRMVLVNGISGAKPTCIBESGHFPDMEADEIFI 252

Search completed: April 13, 2006, 13:00:03

Job time : 42 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.7	32	370	24.5	359	2	Q51426 salmonella
OM protein - protein search, using sw mode1		33	369	24.5	359	2	Q75933 salmonella
Run on:	April 13, 2006, 12:52:23 ; Search time 231 Seconds (without alignments)	34	364	24.1	401	2	Q58C8 trypanosoma
Title:	US-10-686-490D-2	35	359	23.8	279	2	P77026 escherichia
Perfect score:	1509 1 MAQVKANGITITLEYEEQGHRH.....ERHPPRLIELIAGHAAEAER 294	36	358	23.7	280	2	Q8rk2 shigella so
Sequence:	BLOSUM62	37	357	23.7	337	2	Q4qe50 leishmania
Scoring table:	Gapop 10.0 , Gapext 0.5	38	351	23.3	356	2	Q73x9 bacillus ce
Searched:	2166443 seqs, 705528306 residues	39	349	23.1	287	2	Q63a5 bacillus ce
Total number of hits satisfying chosen parameters:	2166443	40	344	22.8	287	2	Q6hh23 bacillus th
Minimum DB seq length: 0		41	344	22.8	287	2	Q81pr3 bacillus an
Maximum DB seq length: 2000000000		42	343	22.7	390	2	Q4qe86 leishmania
Post-processing: Minimum Match 0%		43	336	22.3	284	2	Q81cl3 bacillus ce
Post-processing: Maximum Match 100%		44	335	22.2	279	2	Q98fh3 rhizobium 1
Listing first 45 summaries		45	331	21.9	356	2	Q4mkd6 bacillus ce
Database :	UniProt 05.00:*						
	1: uniprot_sprot:*						
	2: uniprot_trembl:*						
ALIGNMENTS							
RESULT 1							
Q4TR38_9SPHN PRELIMINARY;							
ID Q4TR38;	AC Q4TR38;	DR 13-SEP-2005 (TREMBLrel. 31, Created)	DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)	DB Probable hydrolase.		
GN ORFNames=ELI0688;	OS Erythrobacter litoralis HTCC2594.	RA Giovannini S.J.; Cho J.-C.; Ferriera S.; Johnson J.; Kravitz S., Halpern A.; Remington K.; Beeson K.; Tran B.; Rogers Y.-H., Friedman R.; Venter J.C.;	RA Friedman R.; Venter J.C.;	RA Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.	CC -1 - CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.		
RN [1]	RP STRAIN=HTCC2594;	DR AAGG01000001; BAL76882.1; -; Genomic_DNA.	DR KW Hydrolase.	CC CC	SEQUENCE 296 AA; 31643 MW; A533C5F39150F1DB CRC64;		
SQ	Best Local Similarity 45.7%; Pred. No. 2e-44;	Best Local Similarity 45.4%; Pred. No. 2e-44;	Indels 99; Gaps 1;	Query Match Score 689; DB 2; Length 296;			
Hydrolase.	Matches 133; Conservative 59; Mismatches 59;	CC	CC	Score 689; DB 2; Length 296;			
SEQUENCE	CC	CC	CC	CC			
QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60	QY 1 MAQVKANGITITLEYEEQGHRHHPSMSLLMLGLGQLIDNPPEIFRGLAERGERFVICPDRDA 60
DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60	DB 1 MPEVATGITHYDDHGPDKADPILLIMFGAQMTLPMELVEALTHGFGFRVTRHDNRDV 60
QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120	QY 61 GLSTKLESVKKENIARYELLASNGLKERVPTYLDDMADTIVGLMDAIGIESTHVGVSMG 120
DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238	DB 121 GMIAQKGDVLRKSIERCLCPCEGTQRQALQSRSVTKLRRIAVPTLVYI 238
QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 121 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240
DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180	DB 121 GMIAQHYAARHDKTKLTSFSTTGPKLPAKKAEALQTATRPSLSBEVIVEGIXKL 180
QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180	QY 181 LTTIGSPG--LDREKLALDVKRVSILTMITSGNPRMPAPRPOVQLQEMRVPKNDKEENIKYNLEL 180
DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 181 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240
QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291	QY 239 SQAEDPLPYQCGRDADHIPSARFELLEGMDHIDPRHIPRLIELTAGHAA 291
DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293	DB 241 HGBDDPLPVPEGRDPAHHGAKITIPGMWHDLPLELVEDLAEEAHAKA 293
QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	QY 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240
DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240	DB 311 SRAIGSPCPASBERLRRVRREGVRSSVPESPTRLSAIVADGRDRMLKSITAPTLVL 240
QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2	QY 280 375.5 24.9 432 2
DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2	DB 280 375.5 24.9 432 2
QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2	QY 280 372 24.7 380 2
DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2	DB 280 372 24.7 380 2
QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2	QY 311 370 24.5 369 2
DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2	DB 311 370 24.5 369 2
QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2	QY 311 364 24.1 364 2
DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2	DB 311 364 24.1 364 2
QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8	QY 311 359.5 23.8 359.5 23.8
DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8	DB 311 359.5 23.8 359.5 23.8
QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7	QY 311 357.5 23.7 357.5 23.7
DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7	DB 311 357.5 23.7 357.5 23.7
QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2	QY 311 356 23.6 356 2
DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2	DB 311 356 23.6 356 2
QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2	QY 311 355 23.5 355 2
DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2	DB 311 355 23.5 355 2
QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2	QY 311 354 23.4 354 2
DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2	DB 311 354 23.4 354 2
QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2	QY 311 353 23.3 353 2
DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2	DB 311 353 23.3 353 2
QY 311 352 23.2 352 2	QY 311 352 23.2 352 2	QY 311 352 23.2 352					

RT oxyR;" ;	DR EMBL; BX950851; CRG75135.1;	DR GO; GO:0016787; F:hydrolase activity; IEA.
RL J. Bacteriol. 181:2925-2928 (1999).	DR InterPro; IPR000073; A/b_hydrolease.	
RN [5]	DR InterPro; IPR000379; Ser_estr_s1.	
RP NUCLEOTIDE SEQUENCE.	DR Pfam; PF00561; Abhydrolase_1;	
RX PubMed=15514110; DOI=10.1093/nar/gkh910;	KW Complete proteome; Hydrolase.	
RA Barbe V., Valenet D., Ponknechten N., Kreimeyer A., Oztaas S.,	SEQUENCE 306 AA;	Score 33739 MW; 5A0F2C613F6B5B2 CRC64;
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker B.,	Query Match 38.4%; Score 579; DB 2; Length 306;	
RA Ornston L.N., Weissenbach J., Mariere P., Cohen G.N., Medigue C.;	Best Local Similarity 43.9%; Pred. No. 5..3e-36;	
RT "Unique features revealed by the genome sequence of Acinetobacter sp. ADP1, a versatile and natural transformation competent bacterium.";	Mismatches 45;保守性 105; Indels 6; Gaps 3;	
RT Nucleic Acids Res. 32:5766-5779 (2004).	Matches 122; Conservative 45; Mismatches 45; Indels 6; Gaps 3;	
RL EMBL; Z48863; CAAB8927.1; -; Genomic_DNA.	Qy 4 VRANGITLVEEGQRHHRPSMLLIMGLQQLDWPFFIRGLAERGPFRVICFDNRDAGLS 63	
DR PIR; S57530; S57530.	Db 5 IRNGVNNTAYESGDESETEIIILVAGLGSQMSWSDACOTVUSRGYVIRFDHDVGCS 64	
DR GO; GO:0016787; F:hydrolase activity; IEA.	64 TKLEGVKKPNIAARVFLASMGLKPRVPYTLDDMALTIVGLMDALGTESTHVVGVSMGGNI 123	
DR InterPro; IPR000073; A/b_hydrolease.	65 SHYDSPVNPENIGEVNKAISANRDPVSTLDDAGDLIGLMDAISTAHFVGRSGGNI 124	
DR InterPro; IPR000379; Ser_estr_s1.	66 LEGV_KKPNIAARVFLASGCL-KERVPTLDDMALTIVGLMDALGTESTHVVGVSMGGNI 123	
DR Pfam; PF00561; Abhydrolase_1; 1.	67 TGTGKPLVQCGCRDIAHDHPIGARFELIEGMGHIDIPER 276	
Complete proteome; Hydrolase.	Db 124 AQILGAKHGERVSLTMITSGNPNRMPAPRPPVQLKEMRVPKS--MDKEEWNKNUBL 180	
SEQUENCE 312 AA;	Db 125 AQIATARIPIPERVLSLIMSSSNPSLPQTADPM-ALMTOPPNPFINEPEYLHRL 183	
Score 58.5%; DB 2; Length 312;	Qy 181 LTIGSP-GLDBEKLAUDVRKSIERCLCPGTQRLAALLOGSRSVLLRRAVPTLV 238	
Best Local Similarity 45.5%; Pred. No. 8..6e-37;	Db 184 AERLAGKTYPFDTERTYRSQKEELRRCENPENGFTRQNALVASGDRRKLLATIAAPTLYI 243	
Matches 130; Conservative 53; Mismatches 100; Indels 3; Gaps 3;	Qy 185 QGAEDPILPYQCGCRDIAHDHPIGARFELIEGMGHIDIPER 276	
Qy 6 ANGITLEYERQGRHRRPHPSMLLIMGLGGQQLDWPFFIRGLAERGPFRVICFDNRDAGLS 65	Db 244 HGDDPLFVPSHGEDVAINIPERFMLIDGMGHIDIPNQ 281	
Db 24 SNGLRLHVVGGNPDPHTILLIMGLQALFWPDFFCKSLIDQGFYVTFNDRDIGLSK 83	RESULT 6	
Qy 66 LEGV_KKPNIAARVFLASGCL-KERVPTLDDMALTIVGLMDALGTESTHVVGVSMGGNI 123	Qy 186 QSYH40_PSEA PRELIMINARY; PRT; 328 AA.	
Db 84 TRHKSKRKLANTKLMSRFTGLGNQCAPTYDMDAEDVSLEAMRKICNVNIGASMGGNI 143	Db 187 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Qy 124 AQILGAKHGERVSLTMITSGNPNRMPAPRPPVQLKEMRVPKS--MDKEEWNKNUBL 183	Db 188 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Db 144 AQIATAKYYPKVKERKALMFTSNNPQLPPLPPKOLFSLICKPKSSDEODGILNSLKLFEI 203	Db 189 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Qy 184 IGSPGLDRBKLAUD-VRKSTERCLCPGTQRLAALLOGSRSVLLRRAVPTLV 242	Db 190 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Db 204 IGSPSYVNQYEAQTPARKYQRSRTHPAGLQQFLAICLCTGSLLQDKQISQPTLV 263	Db 191 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Qy 243 DPLIUPYQCGCRDIAHDHPIGARFELIEGMGHIDIPERHPIJELJAGH 288	Db 192 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Db 264 DRLLPPSHSKAVAKAIGKAKFKELIQGMGDIPHPHIPOQSYLFARH 309	Db 193 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RESULT 5	Db 194 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
Q6508_ERWC� PRELIMINARY; PRT; 306 AA.	Db 195 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
IC Q6508,"	Db 196 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
AC 06508,"	Db 197 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RC SPTRAIN=ICRI 1043 / ATCC BAA-672;	Db 198 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;	Db 199 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Bell K.S., Sabahina M., Richard L., Holdren M.T.G., Hyman L.J.,	Db 200 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Holeva M.C., Thompson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,	Db 201 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Atkin R., Baton N., Brooks K., Chillingworth T., Clark K., Doggett J.,	Db 202 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Fraser P., Hance Z., Hauser H., Jages K., Moule S., Norbertczak H.,	Db 203 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,	Db 204 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;	Db 205 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RT "Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors";	Db 206 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).	Db 207 QSYH40; PSEA PRELIMINARY; PRT; 328 AA.	

Qy	4 VRKANGITLVEEQGHRHPSMILLIMGLKQOLIDWPEEFTRGLAERGRVIFCDNRDAGL 63	Db	198 IAQHIAAMAPERTVSLLTLYMSSSGAAGLPAAPDPAVQOLLAR-RSAPNREVAEQADILLA 256
Db	31 VELGDYRLAKSIGRSDPALLVWLGQLIRHPEDEVALCEQFPRTRYDNRDAGL 90	Qy	183 TIGSPGL--DREKLALDVRKSIRCLCPEGTOROLAATIQLGSRSVKKLRRIAVPTLVISG 240
Qy	64 TKLEGVKPNTARYFLAASMGLKPKRVPPYTLDDMAALDTVGMLDALGIESTTHVGYSMGEMI 123	Db	257 ALGSPEVRDDEREVLLHQAAQAYDRAFNPGAKQIMAILAEPSRVELLNQLRVETLVVHG 316
Db	91 AWNVVPSSRSLTYEVYRLRGLPVSAAPTLLTDMAGDALHILDAIPQAHVLGASMGMNI 150	Qy	241 AEDPLPTOCGRDIAHDHPGARPELIEGMGHDIPE 275
Qy	124 AQILGAHKGERVKSLTMITSSGGNPRMAPPQVLOKFRPKVSKMDKEEWIKYNNELLT 183	Db	317 TADPLPVNHGVHLAAHIRGSQRLIPGLAHRFQE 351
Db	151 AQHIADMAPPQRLSLTLMITSSGGNPRMAPPQVLOKFRPKVSKMDKEEWIKYNNELLT 209	RESULT 8	
Qy	184 IGSPGL--DREKLALDVRKSIRCLCPETQRQLAALQGSRSVKKLRRIAVPTLVISG 241	Q4K713_PSEFS	
Db	210 IGSPEVRDQOLQAAARSDRATNPETQRQLAALQGSRSVKKLRRIAVPTLVISG 269	ID Q4K713_PSEFS PRELIMINARY;	PRT; 397 AA.
AC	Q8BNY9_PSEPK	AC Q4K713_PSEFS	
AC	Q8BNY9_PSEPK PRELIMINARY;	AC Q4K713_PSEFS	
DT	01-JUN-2003 (TREMBLrel. 24, Created)	DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)	
GN	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)	
OS	Pseudomonas putida (strain K72440).	DE Hydrolyase, alpha/beta fold family.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	GN ORPName=PF1_4889;	
OC	Pseudomonadaceae; Pseudomonas.	OS Pseudomonas fluorescens (strain Pf-5).	
OX	[1]	OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	
OX	NCBI_TAXID=22664;	OC Pseudomonas.	
RN	NCBI_TAXID=22664;	OX NCBI_TAXID=22664;	
RP	NUCLEOTIDE SEQUENCE.	RP NUCLEOTIDE SEQUENCE.	
RX	DOI:10.1046/j.1462-2910.2002.00366.x;	RX DOI:10.1038/nbt110;	
RA	Martins dos Santos V.A.P., Paulsen I.T., Fouts D.B., Gill S.R., Hiltbert H.,	RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,	
RA	Brinkac L.M., Beaman M.J., Debroy R.T., Daugherty S., Kolonay J.F.,	RA Madupu R., Seshadri R., Ren Q., Madupu R., Dodson R.J.,	
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,	RA Durkin S., Brinkac L.M., Daugherty S.A., Rosovitz M.,	
RA	Hance I., Chris Lee P., Holtrapp E.K., Scanlan D., Tran K.,	RA Grinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,	
RA	Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,	RA Khouri H.M., Pierson B., Pierson L., III, Thomasow L., Loper J.;	
RA	Weder H., Lauber J., Strijpandic D., Roheisel J., Straetz M., Heim S.,	RA RT Fluorescens Pf-5;	
RA	Kiewitz C., Eisben J.A., Timmis K.N., Duisterhoeft A., Tuemmler B.,	RL DR Biotechnol. 23:873-878 (2005).	
RA	Fraser C.M., Weinert C., Paulsen I.T.,	DR DR Hydrolase. CP000076; AAY94119.1; -; Genomic_DNA.	
RA	Martins dos Santos V.A.P., Paulsen I.T., Fouts D.B., Gill S.R., Pop M., Holmes M.,	SQ SEQUENCE 397 AA; 42869 MW; 2F7FFD2116P6E86 CRC64;	
RA	Brinkac L.M., Beaman M.J., Debroy R.T., Daugherty S., Kolonay J.F.,	Query Match 37.2%; Score 561.5; DB 2; Length 397;	
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,	Best Local Similarity 45.4%; Pred. No. 1.6e-34;	
RA	Hance I., Chris Lee P., Holtrapp E.K., Scanlan D., Tran K.,	Matches 122; Conservative 43; Mismatches 101; Indels 3; Gaps 2;	
RA	Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,	QY 9 ITLBEYEEQGRHRPHPSMILLIMGLGGQOLIDWPEEFTRGLAERGRVIFCDNRDGLSTKLEG 68	
RA	Weder H., Lauber J., Strijpandic D., Roheisel J., Straetz M., Heim S.,	DB 94 VSLEYQSITGRTSDPALLVMGLGGQOLIDWPEEVVLLCQQGRVIRYDNRDVGLSTVROA 153	
RA	Kiewitz C., Eisben J.A., Timmis K.N., Duisterhoeft A., Tuemmler B.,	RT 69 VKKPNIARVFLASLMSGLKPRVPTYDLDNALDVTGLMAGLISSTHVVGSMGMIQLG 128	
RA	Fraser C.M., Weinert C., Paulsen I.T.,	DR 154 PYSANLPEEVLYKLGPVAAYTTLDMADDALGLMDALHICOFHVNLGASMGMIQHLA 213	
RA	Martins dos Santos V.A.P., Paulsen I.T., Fouts D.B., Gill S.R., Pop M., Holmes M.,	DR GO:0016787; F: hydrolyase activity; IEA.	
RA	Brinkac L.M., Beaman M.J., Debroy R.T., Daugherty S., Kolonay J.F.,	DR GO:0016740; F: transferase activity; IEA.	
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,	DR InterPro; IPR000073; A/b hydrolase.	
RA	Hance I., Chris Lee P., Holtrapp E.K., Scanlan D., Tran K.,	DR InterPro; IPR000073; Ser esterase.	
RA	Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,	DR Pfam; PF0561; Abhydrolase_1.	
RA	Weder H., Lauber J., Strijpandic D., Roheisel J., Straetz M., Heim S.,	KW Complete Proctome; Hydrolase; Sequence 378 AA; 41119 MW; 055BABDF98F3BBA CRC64;	
RA	KW	Query Match 37.3%; Score 562.5; DB 2; Length 378;	
RA	Fraser C.M., Weinert C., Paulsen I.T.,	Best Local Similarity 44.4%; Pred. No. 1.3e-34;	
RA	Martins dos Santos V.A.P., Paulsen I.T., Fouts D.B., Gill S.R., Hiltbert H.,	Matches 122; Conservative 47; Mismatches 103; Indels 3; Gaps 2;	
RA	Brinkac L.M., Beaman M.J., Debroy R.T., Daugherty S., Kolonay J.F.,	QY 247 PYOGRDIAHDHPGARPELIEGMGHDIPE 275	
RA	Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,	DB 273 VSDDRQVLLQQAAVAVYRAFNPPEGVTKQIMAILAEPSRVALLQQLRVPTLVVHGTDPL 332	
RA	Hance I., Chris Lee P., Holtrapp E.K., Scanlan D., Tran K.,	RESULT 9	
RA	Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,	Q97TK4_CLOAB PRELIMINARY;	
RA	Weder H., Lauber J., Strijpandic D., Roheisel J., Straetz M., Heim S.,	AC Q97TK4_CLOAB	
RA	Kiewitz C., Eisben J.A., Timmis K.N., Duisterhoeft A., Tuemmler B.,	DR 01-OCT-2001 (TREMBLrel. 18, Created)	
RA	Fraser C.M., Weinert C., Paulsen I.T.,	DR 01-OCT-2001 (TREMBLrel. 18, Last sequence update)	
RA	Martins dos Santos V.A.P., Paulsen I.T., Fouts D.B., Gill S.R., Hiltbert H.,	DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	

DR	Pfam; PF00561; Abhydrolase_1.	Db	114 QIDGQLPRISQLKNNMMLQTLGLSNKGTVAYNLTDMAEDTARLILKALQLSKTHLIGASMGCG 173	
KW	Complete proteome; Hydrolase.	SQ	Complete proteome; Hydrolase.	
SEQUENCE	330 AA; 38535 MW; 7010B01ED2666CA1 CRC64;	Query Match	Score 548 5%; DB 2; Length 330;	
Best Local Similarity	44.6%; Pred. No. 1.3e-33;	Mismatches	43; Mismatches 103; Indels 3; Gaps 2;	
Matches	120; Conservative	9 ITILEYPEQGHHRHPSMILNGKLLDWPPEPTECLAREGPERVICPDNDAGLSTKLES 68	Db	122 MIQIGAKHGKGERVKSILIMITSSGNPMPAPRPOVLOKEFMRVPSMKEEWWTKYNLEL 181
Qy	36 VRIATQSIGSESDPAIYLNGGGOLIHWDDEVVAAQCQGYRTYRDVGELSTMVQ 95	Db	124 MIAQIGAKHGKGERVKSILIMITSSGNPMPAPRPOVLOKEFMRVPSMKEEWWTKYNLEL 181	
Qy	69 VRKPNTIARVFILASMLKLPRVPTYDLMALDTVGIMDAQJESTHVG(SMGGMIAQ)LG 128	Db	182 TTGSPGDLREKLAQDVK-S-TERC1CPEGTORQLAALIQLSGSRVLRRIAVPFLVSG 240	
Db	96 PADANITVEVRYKLGLPVSSPSYSLTDMDAAGLMDAQIQRPHVLGSMSGMIAQHL 155	Db	234 KTVGTPGHNVNMYRDIAKIPYQNRHPLGTVQNLASSISREFQKVAPTIVLHG 293	
Qy	129 AKHGERVKSLTLMITSGGNPRMPAPRPOVLOKEFMRVPSMKEEWWTKYNLELTTIGSG 188	Db	241 AEDFLPYQCGRDIAHDHPGARFELIEGMGDIPERHHPRLBLAGH 288	
Db	156 DLAPSNSPESTLIMTSGGAOGLPMPNAALQQLLAR-RGAAPDREVALEQADLLAALGSPQ 214	Db	294 SADGLLPASQGRVVAKTIPNAKEPHLIGEMAHDPETYTOPYMDLISNH 341	
Qy	189 L-DREKLAQDVKSIERCLCPESTQORQLAALQSGSRVLRRIAVPFLVISQAEDL 246	RESULT 13	Q4ZPH7_PSESY PRELIMINARY; PRT; 330 AA.	
Db	215 VKDDEQQLHQAAVSYDRATNPPEGTYKROQMAILAEPSPRVELLNLRLPFLVWHTGADPL 274	AC	Q4ZPH7_PSESY PRELIMINARY; PRT; 330 AA.	
Qy	247 PYQCGRDIAHDHPGARFELIEGMGDIP 275	DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)	
Db	275 PVMGHVVAHHIQGSQRLIPGLAHRFQ 303	DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)	
Qy	345 AA.	DE	Alpha/beta hydrolase fold precursor.	
Db	345 AA.	GN	ORFNames=Psy; 39195;	
Qy	345 AA.	OS	Pseudomonas syringae pv. syringae B728a.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	
OX	Pseudomonadaceae; Pseudomonas.	OC	Pseudomonadaceae; Pseudomonas.	
RN	[1]	NCBI_TAXID=205918;	NCBI_TAXID=205918;	
RP	NUCLEOTIDE SEQUENCE.	RN	[1]	
RC	STRAIN=B728a;	RP	NUCLEOTIDE SEQUENCE.	
RG	DOE Joint Genome Institute;	RC	STRAIN=B728a;	
RA	Chain P., Larimer F., Di Bartolo G., Copeland A., Lykidis A., Trong S.,	RG	Feil H., Peil W.S., Lindow S.E.;	
AC	Goltsman E., Thiel J., Maloffati S., Lapidus A., Detter J.C.,	RA	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
DT	Nolan M., Goltsman E., Thiel J., Maloffati S., Lapidus A., Detter J.C.,	RA	Land M., Richardson P.M., Kyriakis N.C., Ivanova N.;	
DT	13-SEP-2005 (TREMBLrel. 31, Last sequence update)	RT	"Comparison of two complete genome sequences of Pseudomonas syringae	
DT	13-SEP-2005 (TREMBLrel. 31, Last annotation update)	RT	pv. syringae B728a and pv. Tomato DC300.";	
DB	Probable alpha/beta hydrolase fold family esterase.	RL	Proc. Natl. Acad. Sci. U.S.A. 0:0 (2005);	
GN	ORFNames=Psy; 1191;	RN	[2]	
OS	Psychrobacter arcticum 273-4.	RP	NUCLEOTIDE SEQUENCE.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	RC	STRAIN=B728a;	
OC	Moraxellaceae; Psychrobacter.	RA	Loper J.;	
RN	[1]	RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
RP	NUCLEOTIDE SEQUENCE.	RN	[3]	
RC	STRAIN=B728a;	RP	NUCLEOTIDE SEQUENCE.	
RG	NASA Astrobiology Institute;	RC	STRAIN=B728a;	
RA	Ayala-del Rio H.L., Ponder M.A., Di Bartolo G., Ivanova N.,	RA	Feil H., Peil W.S., Lindow S.E.;	
RA	Bergholz P.W., Hauser L., Land M., Batermans C., Rodrigues D.,	RA	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
RA	Klappendieck J.A., Zarka D., Larimer F., Richardson P., Thomasashow M.P.,	DR	EMBL; CP000075; AAY39945.1; -; Genomic DNA.	
RA	Tiedje J.M.;	DR	GO:10016787; F: hydrolase activity; IEA.	
RT	"Complete sequence of Psychrobacter arcticum 273-4";	KW	Hydrolase; Signal.	
RT	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.	FT	SIGNAL 330 AA; 35867 MW; 412D1747A984CDFA CRC64;	
RL	[2]	SEQUENCE	Potential.	
SQ	NUCLEOTIDE SEQUENCE.	Q2	Query Match 35.8%; Score 540.5%; DB 2; Length 330;	
RP	STRAIN=273-4;	AC	Best Local Similarity 43.3%; Pred. No. 5.1e-33;	
RC	RA	Matches 120; Conservative 47; Mismatches 103; Indels 5; Gaps 3;		
RA	Hammon N., Israeni S., Chain P., Di Bartolo G., Ivanova N., Hauser L.,	Qy	1 MAGVKANGITLVEBQGRHRHPSMLIMGLGQOLIDWPEEPFIRGLAERGFRVICDNRD 60	
RA	Land M., Larimer F., Pitluck S., Richardson P.,	DB	30 MANIK-DVRIAYOSITESSDPALLVNGGGOLINHPDEVVVALCQCGYTRYDNRDV 87	
RA	Klappendieck J.A., Zarka D., Larimer F., Richardson P., Thomasashow M.P.,	Qy	61 GISTKLEGVKPNIARYFLLASNLGKIPRVPYTLDDMALDTVGIMDALGIESTHVGSMG 120	
RA	Tiedje J.M.;	DB	88 GLSSWVOOPADANLTENVLYKGLPYSAPVSLTDMADDALGLMDALQIROPHVFLGASM 147	
RA	"Complete sequence of Psychrobacter arcticum 273-4";	Qy	121 GMIAQILGAKHGKGERVKSILIMITSSGNPMPAPRPOVLOKEFMRVPSMKEEWWTKYNLEL 180	
RA	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.	DB	148 GMIAQILGAKHGKGERVKSILIMITSSGNPMPAPRPOVLOKEFMRVPSMKEEWWTKYNLEL 206	
RA	Hydrolase.	Qy	181 LTIGSPGL-DREKLAQDVKSIERCLCPEGTORQLAALOSGRVLRRIAVPFLV 238	
SEQUENCE	345 AA; 38598 MW; 2CB7D61BA536C209 CRC64;	DB	54 DGIELCVAEGPNPNPLLIMGLGQOLIDWPEEPFIRGLAERGFRVICDNRD 113	
RN	NUCLEOTIDE SEQUENCE.	Qy	66 -LEGVKPNIARYFLLASNLGKIPRVPYTLDDMALDTVGIMDALGIESTHVGSMG 121	
RC	STRAIN=273-4;	DB	207 LANLSPQVKDRQQLHQAAVSYDRAFNPEGVTRQIMAILAEPSRVELLNLRLPVLV 266	

Qy	239	SGAEDPLPYOCGRDIAHDHPGARFELJEGMGHDIPE	275																		
Db	267	HGTADPLPVMSVVAHIOGSQRLLPGLAHRFQ	303																		
RESULT 14																					
Q4J684	A2OYI	SGAEDPLPYOCGRDIAHDHPGARFELJEGMGHDIPE	275																		
ID	Q4J684	_AZOVI PRELIMINARY;	PRT;	328 AA.																	
AC	Q4J684																				
DT	13-SEP-2005	(TREMBLrel.	31; Created)																		
DT	13-SEP-2005	(TREMBLrel.	31; Last sequence update)																		
DT	13-SEP-2005	(TREMBLrel.	31; Last annotation update)																		
DB	Alpha/beta hydrolase fold Precursor.																				
GN	AvinDRAFT_8586;																				
OS	Azotobacter vinelandii AvOp.																				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Azotobacter.																				
OC	NCBI_TaxID:322710;																				
RN	NCBI_TaxID:5691;																				
RP	RN																				
RC	RN																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	US DOB Joint Genome Institute (JGI-ORNL); Larimer F., Land M., Palmer P., "Annotation of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.																				
RL	[4]																				
RN	NUCLEOTIDE SEQUENCE.																				
RC	STRAIN=AvOp;																				
RG	US DOB Joint Genome Institute (JGI-ORNL);																				
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israeni S., Pitlick S., Richardson P.; "Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp"; Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.																				
RT	[3]																				
RV	NUCLEOTIDE SEQUENCE.																				
RA	STRAIN=AvOp;																				
RA	DOB Joint Genome Institute; DOB Joint Genome Institute; Submitted (FEB-2003) to the EMBL/GenBank/																				

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,931A
 CURRENT FILING DATE: 1999-02-18
 PRIORITY APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 21999
 LENGTH: 422
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-21999

Query Match Score 37.3%; DB 2; Length 422;
 Best Local Similarity 43.1%; Pred. No. 3.5e-52;
 Matches 125; Conservative 45; Mismatches 117; Indels 3; Gaps 2;
 Qy 4 VKANGITLVEEQGHRHPSMLIMGLGGQOLIDWPEEFIRGLAERGRFVICFDNRDAGIS 63
 Db 125 VELGDVRLAQSIGDSDPALLNGLGQLIHPDEVSCEQGFRTRIDNRDGLS 184
 Qy 64 TKLEGVKPNIARYFLASMLGKPRVPTLDDMADLTGMLDALGIESTHVGVSMGMI 123
 Db 185 AWNPVPSSRLTYEVRYLGLPVSAVTLDMDALHLDIPOAHVLGASMGM 244
 Qy 124 AQILGAKHGERVSLTLMATSGNPRMPAPRQVLTQKFMRVPKSMDEKEWIKYNLELLT 183
 Db 245 AQHADMAPRLLSLTWNSSGAEGLPAPSESULRLL-REAAQDAVEQADLIA 303
 Qy 184 IGSPRL--DREKLALDVRSKIERCLCPECTORQDAILQSGSRVLLRRAVPTLVSGA 241
 Db 304 LGSPEVRDRDQQLIQAASYSYDRAFNPGVQRQIAILAEPSRVPLRLQVPTLVHG 363
 Qy 242 EDPLLPYQCGRDIAHDHIGARFELTEGMHDPERHPIPLIELJAGHAA 291
 Db 364 ADPLLPVMEGVHVAHRSSELKJPGLHRFQEAFKEPLLAAVVPUKA 413

RESULT 3
 US-09-540-236-3609
 Sequence 3609, Application US/095402336
 Patent No. 6673310
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 FILE REFERENCE: 2709.2005-001
 CURRENT APPLICATION NUMBER: US/09/540,236
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO: 3609
 LENGTH: 360
 TYPE: PRT
 ORGANISM: *M.catarrhalis*
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (250)
 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
 US-09-540-236-3609

Query Match Score 32.0%; DB 2; Length 360;
 Best Local Similarity 37.3%; Pred. No. 1.1e-43;
 Matches 107; Conservative 61; Mismatches 113; Indels 6; Gaps 3;

Qy 8 GITLBYEEQGHRHPSMLIMGLGGQOLIDWPEEFIRGLAERGRFVICFDNRDAGLSK- 65
 Db 42 GIKLKVCAEGCNPPMIPMTGTTGMLDALGIESTHVGVSMGMI 101
 Qy 66 LEGYRKPNIARYFLASMLGKPR---VPVTDMDALDTGMLDALGIESTHVGVSMGMI 122
 Db 102 IDGLPLRNLTPKOMLKMQAGLSNRSEPVAYLTDMAEDARLKTMOHLNVNLIGASNGM 161

RESULT 4
 US-08-935-263-10
 Sequence 10, Application US/08935263A
 Patent No. 6117669
 GENERAL INFORMATION:
 APPLICANT: Furuchi, Yasuhiro
 APPLICANT: Hoshino, Tatsuo
 APPLICANT: Kimura, Hitoshi
 APPLICANT: Kiyasu, Tatsuya
 TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 CURRENT APPLICATION NUMBER: US/08/935,263A
 CURRENT FILING DATE: 1997-09-22
 EARLIER APPLICATION NUMBER: EP 96115540.5
 EARLIER FILING DATE: 1996-09-27
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 10
 LENGTH: 267
 PRT
 ORGANISM: Kurthia sp.
 US-08-935-263-10

Query Match Score 20.8%; DB 2; Score 314.5%; DB 2;
 Best Local Similarity 33.1%; Pred. No. 1.3e-25;
 Matches 92; Conservative 43; Mismatches 14; Indels 39; Gaps 9;
 Qy 1 MAQVKANGITLVEEQGHRHPSMLIMGLGGQOLIDWPEEFIRGLAERGRFVICFDNRDAG 60
 Db 1 MPFVNHNDESYEV--HGQGDPILLINGLGYNLSNW-HRTVFLAQR-FKVTFDQRGV 56
 Qy 61 GLSTKLEGVKPNIARYFLASMLGKPRVPTLDDMADLTGMLDALGIESTHVGVSMG 120
 Db 57 GSNS-----REQPQPSIEMMAEDARAVLDVSVDSAHVYGSMG 95
 Qy 121 GMIAQILGAKHGERVSLTLMATSGNPRMPAPRQV--LOKFMRVPKSMRKEEW---- 173
 Db 96 GMIAQRQLITYPERSVSLVLCGTAGTTHQSPPESTLMSRASLTGSPRDNWLAAP 155
 Qy 174 IKYNLELLITTCGPDREKLALDVRSKIERCLCPECTORQDAILQSGSRVLLRRAV 233
 Db 156 IVYSQATEK--HPELIQE---DQKRRIITPPSAYLSQQUACLTHDTSNS-LDKINI 208
 Qy 234 PTLVISGAEDPLLPYQCGRDIAHDHIGARFELIEGMCH 271
 Db 209 PTLIIHGDADNLVPPYENGKMLAERIQQSQQHTVSCAGH 246

RESULT 5
 US-09-540-185-10
 Sequence 10, Application US/09594185
 Patent No. 6365388
 GENERAL INFORMATION:
 APPLICANT: Furuchi, Yasuhiro
 APPLICANT: Hoshino, Tatsuo
 APPLICANT: Kimura, Hitoshi
 APPLICANT: Kiyasu, Tatsuya
 APPLICANT: Nagashashi, Yosbie

1 TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 FILE REFERENCE: Biotin Genes
 CURRENT APPLICATION NUMBER: US/09/594,185
 CURRENT FILING DATE: 2000-08-14
 PRIORITY NUMBER: 08/935,263
 PRIOR APPLICATION NUMBER: 08/935,22
 PRIOR FILING DATE: 1997-09-22
 PRIORITY NUMBER: EP 96115540.5
 PRIORITY NUMBER: EP 96115540.5
 NUMBER OF SEQ ID NOS: 23
 SEQ ID NO: 10
 LENGTH: 267
 TYPE: PRT
 ORGANISM: Kurthia sp.
 US-09-594-185-10

Query Match 20.8%; Score 314.5; DB 2; Length 267;
 Best Local Similarity 33.1%; Pred. No. 1.3e-25;
 Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 7
 US-10-763-933-10
 1 MAQVKANGTLELEYEQGRHRPHSPMLLIMGLGGQLIDWPBEFIRLAERGFRVICFDNRDA 60
 ; Sequence 10, Application US/10763933
 ; Patent No. 6955906
 ; GENERAL INFORMATION:
 ; APPLICANT: Furuchi, Yasuhiro
 ; APPLICANT: Hoshino, Tatsuo
 ; APPLICANT: Kimura, Hitoshi
 ; APPLICANT: Nagahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; CURRENT APPLICATION NUMBER: US/10/763,933
 ; CURRENT FILING DATE: 2004-01-23
 ; PRIOR APPLICATION NUMBER: US/10/033,078
 ; PRIOR FILING DATE: 2001-12-27
 ; PRIOR APPLICATION NUMBER: 09/594,185
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: EP 96115540.5
 ; PRIOR FILING DATE: 1996-09-27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; NUMBER OF SEQ ID NOS: 23
 ; SEQ ID NO: 10
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.

Query Match 20.8%; Score 314.5; DB 2; Length 267;
 Best Local Similarity 33.1%; Pred. No. 1.3e-25;
 Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 6
 US-10-033-078-10
 1 Sequence 10, Application US/10033078
 ; Patent No. 672354
 ; GENERAL INFORMATION:
 ; APPLICANT: Furuchi, Yasuhiro
 ; APPLICANT: Hoshino, Tatsuo
 ; APPLICANT: Kimura, Hitoshi
 ; APPLICANT: Kiyasu, Tatsuya
 ; APPLICANT: Nagahashi, Yoshie
 ; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 ; FILE REFERENCE: Biotin Genes
 ; CURRENT APPLICATION NUMBER: US/10/033,078
 ; CURRENT FILING DATE: 2001-12-27
 ; PRIOR APPLICATION NUMBER: 09/594,185
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR FILING DATE: 1996-09-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 10
 ; LENGTH: 267
 ; TYPE: PRT
 ; ORGANISM: Kurthia sp.
 US-10-033-078-10

Query Match 20.8%; Score 314.5; DB 2; Length 267;
 Best Local Similarity 33.1%; Pred. No. 1.3e-25;
 Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 8
 1 MAQVKANGTLELEYEQGRHRPHSPMLLIMGLGGQLIDWPBEFIRLAERGFRVICFDNRDA 60

US-09-902-540-14883
i Sequence 14883, Application US/0902540
i Patent No. 68333447
i GENERAL INFORMATION:
i APPLICANT: Goldman, Barry S.
i APPLICANT: Hinkle, Gregory J.
i APPLICANT: Slater, Steven C.
i APPLICANT: Wiesand, Roger C.
i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
i FILE REFERENCE: 38-10(15849)B
i CURRENT APPLICATION NUMBER: US/09/902,540
i CURRENT FILING DATE: 2001-07-10
i PRIOR APPLICATION NUMBER: 60/217,883
i PRIOR FILING DATE: 2000-07-10
i NUMBER OF SEQ ID NOS: 16825
i SEQ ID NO 14883
i LENGTH: 247
i TYPE: PRT
i ORGANISM: Myxococcus xanthus
i US-09-902-540-14883

Query Match 17.4%; Score 262.5; DB 2; Length 247;
 Best Local Similarity 30.3%; Pred. No. 5.1e-20;
 Matches 79; Conservative 38; Mismatches 107; Indels . 37; Gaps 7;

Qy 45 LAERGFRVTCRVDLSTKLEGVKPKNIAVRFLASGLKPRVPYTDLMDALTVGL 104
 Db 4 LARAGRFVRYDRLDTGRS-----SHGVGATPYTDLDAADVSL 45
 Qy 105 DALGIESTHVGVSMMMAQILGAHKHGHRVKSLTLM--ITSSGNPRMPAPRQVTLQKF 161
 Db 46 DGYGTERAHLVGMGSLQLCQLVALKYPRVLSLTISQIPEPDPGMDPAVLAHF 105
 Qy 162 MRVP--KSNDKEENVYKYNBL-LTTIGSP--GLDREKLADYRKTSIERCLCPGTORLA 216
 Db 106 QRAATLAWNSBAAEAGFOVLSRLCVGRARRSFBEARVARA:VODYRRAAPO----C 159
 Qy 217 AIIQSGSRVKL---LRRIAVPPLIVISGAEDPPLPYQCGRDYDHIPCARFELIEGMKH 271
 Db 160 ALNHAGLSCOLEWGRTRTEAIPVLIHSVSDPVTDHAGVALSRAVKGACLYTLHDGH 219
 Qy 272 DIPPERHIPPLIELLAGHAAA 292
 Db 220 DLHFDDEWTMTRAHTSRA 240

Query Match 12.6%; Score 189.5; DB 2; Length 251;
 Best Local Similarity 29.1%; Pred. No. 4.3e-12;
 Matches 76; Conservative 35; Mismatches 99; Indels 51; Gaps 9;

Qy 50 FRVICFDNRDAGLSTKLEGVKPKNIAVRFLASGLKPRVPYTDLMDALTVGLMDALG 109
 Db 1 FRTVIALDRLGFGESSRPSDL-----ADYRFDDAEDLEALLDALGL 41
 Qy 110 ESTHV-YGVSMGGMIAQILGAHK-HGHRVKSLTLMITSSGNPRMPAPRQVQKFMRYPK- 166
 Db 42 DRPVLYGHSMGCAALAYAARYPEERVKALVST-----PAPGLSSRLPRLGNL 94
 Qy 167 -----SMDREWKVNLELLTIGSPGL-DREKLADYRKTSIERCLCPGTQR 213
 Db 95 EGHILLANFNRLSRSEALLGRALKQFFLGCRPFVSVFLKQNBDMWSSLARPGETDGSG 154
 Qy 214 QLAALIOSGSRVK---LLRRIAVPPLIVISGAEDPPLPYQCGRDIAHIDIPGARFELIEGM 269
 Db 155 LIGYAVALGKLLQWDRAALKIKVPTLVWGDPLPLVKASEKLSALFPNAEVVVIDA 214
 Qy 270 GH---DIPERHIPPLIELAGHAAA 286
 Db 215 GHLLALEKPE-EVAELIKFLA 234

Query Match 12.7%; Score 192; DB 2; Length 287;
 Best Local Similarity 26.9%; Pred. No. 2.8e-12;
 Matches 71; Conservative 38; Mismatches 111; Indels 44; Gaps 6;

Qy 6 ANGITLEYEEQGRHRHPSMSLIMGGQOLIDWPPEEFIRGLAERGFYRCIDPNDRAGLSTK 65
 US-09-252-991A-22466
i Sequence 22466, Application US/09252991A
i Patent No. 6551195
i GENERAL INFORMATION:
i APPLICANT: Marc J. Rubenfield et al.
i TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i FILE REFERENCE: 107196-136
i CURRENT APPLICATION NUMBER: US/09/252,991A
i CURRENT FILING DATE: 1999-02-18
i PRIOR APPLICATION NUMBER: US 60/074,788
i PRIOR FILING DATE: 1998-02-18
i PRIOR APPLICATION NUMBER: US 60/094,190
i PRIOR FILING DATE: 1998-07-27
i NUMBER OF SEQ ID NOS: 33142
i SEQ ID NO 22466
i LENGTH: 287
i TYPE: PRT
i ORGANISM: Pseudomonas aeruginosa
i US-09-252-991A-22466

Query Match 12.6%; Score 192; DB 2; Length 287;
 Best Local Similarity 26.9%; Pred. No. 2.8e-12;
 Matches 71; Conservative 38; Mismatches 111; Indels 44; Gaps 6;

Qy 6 ANGITLEYEEQGRHRHPSMSLIMGGQOLIDWPPEEFIRGLAERGFYRCIDPNDRAGLSTK 65
 US-09-252-991A-32242
i Sequence 32242, Application US/09252991A
i Patent No. 65511795

RESULT 11
 US-09-252-991A-32242
i Sequence 32242, Application US/09252991A
i Patent No. 65511795

GENERAL INFORMATION:
 i APPLICANT: Rubenfield et al.
 i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 i FILE REFERENCE: 107196 136
 i CURRENT APPLICATION NUMBER: US/09/252,991A
 i CURRENT FILING DATE: 1999-02-18
 i PRIOR APPLICATION NUMBER: US 60/074,788
 i PRIOR FILING DATE: 1998-02-18
 i PRIOR APPLICATION NUMBER: US 60/094,190
 i NUMBER OF SEQ ID NOS: 33142
 i SEQ ID NO: 32242
 i LENGTH: 268
 i TYPE: PRT
 i ORGANISM: Pseudomonas aeruginosa
 i US-09-252-991A-32242

Query Match 12.5%; Score 189; DB 2; Length 268;
 Best Local Similarity 25.5%; Pred. No. 5.3e-12; Indels 66; Gaps 10;
 Matches 75; Conservative 38; Mismatches 115; Delins 66; Gaps 10;
 Qy 1 LEYEEQGRHRPHPSMILLIMGLGSQLIDWPEEFTRGLAERGPRVICPDNRAGLSTKLEGYR 70
 Db 16 ILYSLSPAGAPVLLNSLNLSGTLDGMWDTQ-IPALTAH-FRVLRYDTRGHGASLYTPG-- 71
 Qy 71 KPNIARVFLLASMGKLPKRVPYPTLDMALDVTGLMDALGISTTHVGSWNSGMMIAQLGAK 130
 Db 72 -----PFAIGOLQGADVLALLDALELPRVHECGLSMCGLIGOWLGH 112
 Qy 131 HGERVTKSLLTMITSS-----GNPMPMPRQVLT---QKFMRVPSKMSMKBEWKYNEL 180
 Db 113 AGERLGRVLVLCNTAAKIASDEVNTRIDT---VKGGEQAMRVLDAYARWF---- 162
 Qy 181 LTTIGSPGLDREKLAUDVRKSIERCUCPECTORQALIQLQSRSVYKLRRIAVPTLVISG 240
 Db 163 --TAGF--AERPAQVERIVMLAATSPQYAANCAAVRDADFR-EQGLHVQAPTIVAG 217
 Qy 241 AEDPLLPYQCRGDIADHIGPARLEBGMGDIPERHPPJELLAGHAAEA 294
 Db 218 SHDAVTPDNARFMQARIADA-----OLVEFAAAHLSNEA 253

RESULT 12
 US-09-902-540-11639
 i Sequence 11639, Application US/09902540
 i GENERAL INFORMATION:
 i APPLICANT: Goldman, Barry S.
 i APPLICANT: Hinkle, Gregory J.
 i APPLICANT: Slater, Steven C.
 i APPLICANT: Wiegand, Roger C.
 i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 i FILE REFERENCE: 38-10/15849/B
 i CURRENT APPLICATION NUMBER: US/09/902,540
 i CURRENT FILING DATE: 2001-07-10
 i PRIOR APPLICATION NUMBER: 60/217,883
 i SEQ ID NO: 11639
 i LENGTH: 265
 i TYPE: PRT
 i ORGANISM: Myxococcus xanthus
 i US-09-902-540-11639

Query Match 12.3%; Score 185; DB 2; Length 265;
 Best Local Similarity 26.7%; Pred. No. 1.4e-11;
 Matches 77; Conservative 38; Mismatches 121; Delins 52; Gaps 9;
 Qy 1 MAQVRAKNGITLLEYEEOGRHRPHPSMILLI-MGLGGQIOWDPEEFTRGLAERGFRVCFDR 58
 Db 1 MLTVTVGVPHYRDG-KSPPVILUHAPBLNGSTFD--KQVRLSGR-YRFIIPDR 54

RESULT 13
 US-09-46-211A-6
 i Sequence 6, Application US/09469211A
 i Patent No. 666054
 i GENERAL INFORMATION:
 i APPLICANT: J. Archer
 i ARCHER, J.
 i TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
 i FILE REFERENCE: 9341-021
 i CURRENT APPLICATION NUMBER: US/09/469,211A
 i CURRENT FILING DATE: 1998-12-22
 i PRIORITY APPLICATION NUMBER: UK 9828660.2
 i PRIORITY FILING DATE: 1998-12-24
 i NUMBER OF SEQ ID NOS: 19
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO 6
 i LENGTH: 289
 i TYPE: PRT
 i ORGANISM: Rhodococcus sp.
 i US-09-46-211A-6

Query Match 12.1%; Score 183; DB 2; Length 289;
 Best Local Similarity 24.3%; Pred. No. 2.7e-11; Mismatches 123; Indels 46; Gaps 9;
 Matches 68; Conservative 43; Delins 123; Gaps 9;

Qy 4 VKGANTILEYEEOGRHRPHPSMILLMGLGQIOWDPEFRGLAERG--FRVICFNDRAG 61
 Db 22 IQAGPYRTRYLHAGDSKSPKTLLHGHITGH---AEAYTRNLRSHEHFNWAIFIGH 77

Qy 62 LSTKLEGVKPNIARVFLLASMGKLPKRVPYPTLDMALDVTGLMDALGISTTHVGSWNSGMMGG 121
 Db 78 YST-----KPDHPLEIKHYIDHQLLDRIGVEKAFSOBLSLG 116

Qy 122 MIAQILGAGHGERVKSLLTMITSSGGNPRMPAPRQVLOKFMRVPSKMSKDE--EWIKYNL 178
 Db 117 WTVQAFADHDPKEYDTRIVLN-TMGCT---MANPOVMERLYTSMEEAKDPSWENVKARL 171

Qy 179 ELL---TTGSPGLDREKLAUDVRKSIERCUCPECTORQALIQLQSRSVYKLRRIAVPTLVISG 231
 Db 172 EWLMADPTWYTDLIRTOAIFQPQDWLKACENNMALQDLTEKRNMTDAT---LNGI 227

Qy 232 AVPTLIVISGAEDPLPYQCRGDIADHIGPARLEBGMGDIPERHPPJELLAGHAAEA 271
 Db 228 TVPANVLTWTKDPSGPVDEAKRASHIPGAKLAIMENCGH 267

RESULT 14
 US-09-446-681-6
 i Sequence 6, Application US/09446681
 i Patent No. 6849442
 i GENERAL INFORMATION:
 i APPLICANT: Archer, John AC
 i APPLICANT: Summers, David K
 i APPLICANT: Roland, Herve J
 i APPLICANT: Powell, Justin AC
 i TITLE OF INVENTION: Biosensor materials and methods

FILE REFERENCE: 0380-P02083-US0
 CURRENT APPLICATION NUMBER: US 09/446,681
 CURRENT FILING DATE: 2000-03-14
 PRIOR APPLICATION NUMBER: PCT/GB98/01893
 PRIOR FILING DATE: 1998-06-29
 PRIOR APPLICATION NUMBER: GB 97136666.7
 PRIOR FILING DATE: 1997-06-27
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 6
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Rhodococcus corallina
 US -09-446-681-6

Query Match 12.1%; Score 183; DB 2; Length 289;
 Best Local Similarity 24.3%; Pred. No. 2.7e-11;
 Matches 68; Conservative 43; Mismatches 123; Indels 46; Gaps 9;

Qy 4 VRANGITLBYEEOGHRHHPSMLLNGLGOLIDWBEFRGLABRG--PRVICPDNRDAG 61
 Db 22 IQAGPYRTYHLAGDSSKPTILLHGITHG---AEAYRNLRHSEHNWALDFIGH 77

Qy 62 LSTKLEGVKKPNIAVFLASMGKPRVPTLDDMADLTVGLMDALGIESTHYVGVSNCG 121
 Db 78 YST-----KPDHPDEIKHYIDHVQLLDAIGYKASFGESLIG 116

Qy 122 MIAQILGARKGERVSLTMITSSGNPRMPAPRPOVLFQMRVKSMDCR--EWIKNL 178
 Db 117 WVTAQFAHDHPEKVDRIVN-TMGET---MANPQYMERLYTLSMEAADPSPWERVKARL 171

Qy 179 ELL---TTRISPGLOREKLAL---DVRKSIERCUCPECTORQOALLSGSRVKLRI 231
 Db 172 EWLADPTWTDLDIRTRQIFQQPDWLKACMMALOLETRGRNMITDAT---LNGI 227

Qy 232 AVPTLVISGAEDPLLPYOCGRDIADHIPGARFELIEGMGH 271
 Db 228 TVPANVLTWTTKDPSPGVDEAKRIASHIPGAKLAINENGH 267

RESULT 15
 US -09-902-540-12298
 Sequence 12298, Application US/09902540
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US 09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO: 12298
 ; LENGTH: 271
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 US -09-902-540-12298

Query Match 12.1%; Score 182.5; DB 2; Length 271;
 Best Local Similarity 26.8%; Pred. No. 2.7e-11;
 Matches 84; Conservative 45; Mismatches 118; Indels 67; Gaps 14;

Qy 1 MAQVKANGTLEYEBOGRRHPSMLLIMCHGGOLDWPEBINGLAERGSERVICEDNRDA 60
 Db 1 MPILQLEESLFEPSG--EGTPVLFHQGSSGRDW-SVAPRLTRGR-HR7VPDARGH 56

Qy 61 GLSTKLEGVKKPNIAVFLASMGKPRVPTLDDMADLTVGLMDALGIESTHYVGVSNCG 120
 Db 57 GRSGKPPGA-----YGVPRFARDIAGLCDALGTGVHVGLSMG 95

APPLICANT: Furuchi, Yasuhiro
 APPLICANT: Hoshino, Tatsuo
 APPLICANT: Kimura, Hitoshi
 APPLICANT: Kiyasu, Tatsuya
 APPLICANT: Nagahashi, Yoshie
 TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 FILE REFERENCE: Biotin Genes
 CURRENT FILING DATE: 2001-12-27
 PRIOR APPLICATION NUMBER: US/10/033,078
 PRIORITY FILING DATE: 1996-09-27
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 10
 LENGTH: 267
 TYPE: PRT
 ORGANISM: Kurthia sp.
 US-10-033-078-10

Query Match 20.8%; Score 314.5; DB 4; Length 267;
 Best Local Similarity 33.1%; Pred. No. 2.9e-23; Mismatches 43; Indels 39; Gaps 9;
 Matches 92; Conservative 43; Gaps 9;

Qy 1 MAQVKANGTILEYBQGRHHPMSMLIMGLGGOLIDWPEEFIRGLAERGFRVICFCDNMDA 60
 Db 1 MPVNHNDNESLYYEV--HGQGDPPLIMGLGNTNSLW-HRTVPTLAKR-FKVTFDNRCV 56
 57 GKSS-
 61 GLSTKLEGVKPNIARVFLASMLKPRVYTLDDMALDTGLMDALGIESTIVGVSMG 120
 Db 57 GKSS-
 61 GLSTKLEGVKPNIARVFLASMLKPRVYTLDDMALDTGLMDALGIESTIVGVSMG 120
 Qy 174 IKYNLELLTTIGSPGLDREKLALDVRKSIERCUCPECTOROLAAILOSSRSVRLRRIAV 233
 Db 156 IVYSAFIEK--HPELIQG---DIQRKIEITTPSAYLSQACLTHTDSNE-LDKINI 208
 96 GMAQRLITYPVRVSLSVLGCTTAGGTTIOPSPESTIMSRASLTGSPRDNWLAAP 155
 Db 209 PTLIHGDADNLVPTENGKMLAERIQSQFTVSCAGH 246

RESULT 4
 US-10-211-028-165
 Sequence 165; Application US/10211028
 Publication No. US20050027113A1
 GENERAL INFORMATION,
 APPLICANT: COBIST PHARMACEUTICALS, INC.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
 FILE REFERENCE: C0B-12 PCT CIP
 CURRENT APPLICATION NUMBER: US/10/211,028
 CURRENT FILING DATE: 2002-07-31
 PRIOR APPLICATION NUMBER: PCT/US02/24310
 PRIOR FILING DATE: 2002-10-25
 PRIOR APPLICATION NUMBER: PCT/US01/32354
 PRIOR FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: 60/310,385
 PRIOR FILING DATE: 2001-08-05
 PRIOR APPLICATION NUMBER: 60/379,866
 PRIOR FILING DATE: 2002-05-10
 NUMBER OF SEQ ID NOS: 170
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 165
 LENGTH: 273
 TYPE: PRT
 ORGANISM: Streptomyces coelicolor

US-10-211-028-165

Query Match 17.8%; Score 268.5; DB 5; Length 273;
 Best Local Similarity 26.8%; Pred. No. 1.5e-18; Mismatches 44; Indels 79; Gaps 10;
 Matches 85; Conservative 44; Gaps 10;

Qy 1 MAQVKANGTILEYBQGRHHPMSMLIMGLGGOLIDWPEEFIRGLAERGFRVICFCDNMDA 56
 Db 1 MPVLTNGIRINYDAPPAGQONA PAVLLONGSGSGRAWHLHQPAVLVAAGFRVISFD 60
 57 NRDAGLSTKLEGVKPNIARVFLASMLKPRVYTLDDMALDTGLMDALGIESTIVGVG 116
 Db 61 NRGIAPSSEECPG----GFIDDLVADTAALVEELRGPCRVAG 99
 Qy 117 VSMGMITAQILGARGHRGRVKSITLMITSSGNP-----RMPAPRQV 157
 Db 100 ISMGAHQAELASRPPDVDRVLMATRA-REDALLEALCRAEMELYDQGIRLPAYEAV 158
 158 LOKFMRV-PKSNDKE---EWKYNRLLTIGSPGLDREKLALDVRKSIERCLCPBGTQ 212
 Db 159 VQAMQNLSPRLDNDVOARDLDV-LELTRSGA-----GYR 194

RESULT 3
 US-10-763-933-10
 Sequence 10; Application US/10763933
 GENERAL INFORMATION:
 APPLICANT: Furuchi, Yasuhiro
 APPLICANT: Hoshino, Tatsuo
 APPLICANT: Kimura, Hitoshi
 APPLICANT: Kiyasu, Tatsuya
 APPLICANT: Nagahashi, Yoshie
 TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
 FILE REFERENCE: Biotin Genes
 CURRENT FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: US/10/763,933
 PRIOR FILING DATE: 2004-01-23
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 10
 LENGTH: 267
 TYPE: PRT
 ORGANISM: Kurthia sp.
 US-10-763-933-10

APPLICANT: Forych, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: BLITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIORITY APPLICATION NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-21
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/230,335
 ; PRIORITY FILING DATE: 2000-09-06
 ; PRIORITY APPLICATION NUMBER: 60/230,347
 ; PRIORITY FILING DATE: 2000-09-09
 ; PRIORITY APPLICATION NUMBER: 60/242,578
 ; PRIORITY FILING DATE: 2000-10-23
 ; PRIORITY APPLICATION NUMBER: 60/253,625
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/267,636
 ; PRIORITY FILING DATE: 2001-02-09
 ; PRIORITY APPLICATION NUMBER: 60/269,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 7814
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 51
 ; LENGTH: 271
 ; TYPE: PRT
 ; ORGANISM: Streptomyces ruineus
 ; US-10-329-079-51

RESULT 5

Query Match 15.1%; Score 227.5; DB 4; Length 271;
 Best Local Similarity 26.9%; Pred. No. 2.2e-14;
 Matches 84; Conservative 47; Mismatches 98; Indels 83; Gaps 13;

Qy 1 MAQYRANGTLELEYEQGHRHPSMILLIMGGQQLIDWPBPFIRGLAERGRFRVCFDNRDA 60
 Db 1 MPTRINGTALDHDRTG-SGPVLLIMGGAAKSAWHLHQVPAVLVAEFTFNTIR - 56

Qy 61 GLSTKLEGTKPKNTIARVFLLASMGLKPR---VPTYTLDDMWALDTVGLMDALGIBETHVYGV 117
 Db 57 -----GVPSSGGPGFTLGDNAADTVGLIEHLGICAVVM 93

Qy 118 SMGGMIAQILGARGCERVKSLTMITLTTGSSGDPMPMA-----PRPOVLRK 160
 Db 94 SLGARVARERTRPDLVSRCVLAAPRANSDRMBAACTAAEIALADSGVTLPYRYAVVR 153

Qy 161 FMR--VPKSM--DKE--ENIKYNNELLTIGSPGLDREKLALDVRKSTERCLCPEGTORQ 214
 Db 154 AMQNSPRTIADDRIADWD-LLEAANDG-PGL-----RTQLE 191

Qy 215 LAAIQSGGSRVKLRRIAVPTLVISGAEDPLPYOCGRDIADHIPGARFELIGMGH-- 271
 Db 192 LSA---ADRGEDLAGITACPRVIAFADDIVAPPHLAKIADALPEADTHVVPDCGHGY 248

Qy 272 -DIPPERHIPRLI 282
 Db 249 LERPDR-VNRLI 259

Qy 225 ---VKLLRRIAYPTLVISGAEDPLPYOCGRDIADHIPGARFELIGMGHDI P 274
 Db 210 ESAFTGLER--PVLVQARQDKVAPYTHGLRAHEGIASRPFVLEDGHAPP 260

RESULT 6

US-10-282-122A-49054

Sequence 4054, Application US/10282122A
 Publication No. US20040029129A1

GENERAL INFORMATION:
 ; APPLICANT: FARNET, Chris
 ; APPLICANT: ZAZOPoulos, Emmanuel
 ; APPLICANT: STAFERA, Alfredo
 ; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 ; FILE REFERENCE: 3002-110S
 ; CURRENT APPLICATION NUMBER: US/10/329,079
 ; CURRENT FILING DATE: 2002-12-24
 ; NUMBER OF SEQ ID NOS: 66

RESULT 7

US-10-329-079-18

Sequence 18, Application US/10329079
 Publication No. US20030198981A1

GENERAL INFORMATION:
 ; APPLICANT: FARNET, Chris
 ; APPLICANT: ZAZOPoulos, Emmanuel
 ; APPLICANT: STAFERA, Alfredo
 ; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 ; FILE REFERENCE: 3002-110S
 ; CURRENT APPLICATION NUMBER: US/10/329,079
 ; CURRENT FILING DATE: 2002-12-24
 ; NUMBER OF SEQ ID NOS: 66

1 SOFTWARE: PatentIn version 3.0
 2 SEQ ID NO 18
 3 LENGTH: 264
 4 TYPE: PRT
 5 ORGANISM: Streptomyces fradiae
 6 US-10-329-079-18

7 Query Match 14.3%; Score 216.5; DB 4; Length 264;
 8 Best Local Similarity 25.8%; Pred. No. 2.9e-13;
 9 Matches 79; Conservative 44; Mismatches 104; Indels 79; Gaps 10;

10 QY 5 KANGITLEYEBCGHRHPSMILLIMLGCGQOLIDWPEEFIRGLAERGRFVICFDNRDAGLST 64
 11 DB 4 RINGIDLDHERRG-SGSFPVLLIMSGSAAGTGWHLHQTPALVAAGFEAVTFNRR----- 55
 12 QY 65 KLEGVKKPNIARVFLLAASNLKER--VPTYLDDMALDTVGMLDALGEESTHVGVSNGG 121
 13 DB 56 KLEGVKKPNIARVFLLAASNLKER--VPTYLDDMALDTVGMLDALGEESTHVGVSNGG 121
 14 QY 122 MIAOILGAKHGGERVKSUTLMITSGNPMPMA-----PRPOVLOKEMR- 163
 15 DB 97 RVACEVATRDPVLISRCVYLMAPPADTRAATEAEALADS GTVBPYRRAVVRAMQN 156
 16 QY 164 -VPKSMOKKEEWIKYNEL-LITIGSPGLDREKLADIVRSKIERCLCPEGTQBLAALIQ 220
 17 DB 157 LSPTLADDERLADWDLFELAAAAGPG--ARTOLEISAVYH 196
 18 QY 221 SGSEVVKLRLRAVPTLVISGAEDPPLPVQCGRDIAHDHPGARFELIBGMH---DIPER 276
 19 DB 197 --REEDLARIAPCRVIAFADDIVAPAHIAKETADALPDHYVFDGHCYCLEPDR 253
 20 QY 277 HIPRLI 282
 21 DB 254 -VNRLI 258

22 RESULT 8
 23 US-09-976-059-10
 24 ; Sequence 10, Application US/09976059
 25 ; Patent No. US0020164747A1
 26 ; GENERAL INFORMATION:
 27 ; APPLICANT: Farinet, Chris
 28 ; APPLICANT: Zazopoulos, Emmanuel
 29 ; APPLICANT: Staffa, Alfredo
 30 ; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
 31 ; FILE REFERENCE: 3019-PCT
 32 ; CURRENT APPLICATION NUMBER: US/09/976,059
 33 ; CURRENT FILING DATE: 2001-10-15
 34 ; NUMBER OF SEQ ID NOS: 34
 35 ; SOFTWARE: PatentIn version 3.0
 36 ; SEQ ID NO 10
 37 ; LENGTH: 271
 38 ; TYPE: PRT
 39 ;
 40 ; FEATURE: Actinoplanes sp.
 41 ; NAME/KEY: misc_feature
 42 ; LOCATION: (1).
 43 ; OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that
 44 ; other synthesized protein will have a formylmethionine residue
 45 ; OTHER INFORMATION: at this position
 46 ; US-09-976-059-10

47 Query Match 13.5%; Score 204; DB 3; Length 271;
 48 Best Local Similarity 25.0%; Pred. No. 5.6e-12;
 49 Matches 78; Conservative 38; Mismatches 120; Indels 76; Gaps 9;

50 QY 64 TLEGVKKPNIARVFLLAASNLKER--VPTYLDDMALDTVGMLDALGEESTHVGVSNGG 123
 51 DB 62 ----GTPPSDV----PAGCYSLAAMTADPFRGLALDAPICRVIAFADDIVAPAHIAKETADALPDHYVFDGHCYCLEPDR 298
 52 ;
 53 ; Sequence 4, Application US/09976057
 54 ; US-09-976-059-4
 55 ; Sequence 4, Application US/09976057
 56 ;
 57 ; RESULT 10

Patent No. US2002007710A1
 GENERAL INFORMATION:
 - TITLE OF INVENTION: 32225, A NOVEL HUMAN APIHA BETA HYDROLASE
 - APPLICANT: Meyers, Rachel A. ; FAMILY MEMBER
 - TITLE OF INVENTION: AND USES THEREOF
 - FILE REFERENCE: 10448-073001
 - CURRENT FILING DATE: 2001-06-29
 - PRIORITY APPLICATION NUMBER: US/09/896,578
 - PRIORITY FILING DATE: 2000-06-29
 - PRIORITY FILING DATE: 2000-06-29
 - NUMBER OF SEQ ID NOS: 8
 - SOFTWARE: FastSEQ for Windows Version 4.0
 - SEQ ID NO: 4
 - LENGTH: 232
 - TYPE: PRT
 - ORGANISM: Artificial Sequence
 - FEATURE:
 - OTHER INFORMATION: consensus sequence
 US-09-896-578-4

Query Match 13.1%; Score 198; DB 3; Length 232;
 Best Local Similarity 31.5%; Pred. No. 1.9e-11;
 Matches 82; Conservative 36; Mismatches 90; Indels 52; Gaps 12;

Qy 50 PRVICFDNRDAGLSTKLEGVKPKNIARYFLLASMGLKPRVPYPTIDDMALDTVGIMDALGI 109
 Db 1 FRYVLDLRFGESSPSD-----LAE-----YRFDLDAEDLEALLDALGL 40
 Qy 110 ESTHV-VGVSMGGMAQILGAKHGE-RVKSLTIMITSSGNPRM-----PRPVQLK 160
 Db 41 EKPVILVGHSMGGAAIAYAKYPELRYKALVLV-----SPPLPAGLSSDLFRQGNLEG 95
 Qy 161 FM-----RVPKSMDKEEWMKVNLLTITGSPGU-DREKLALDVRKSSTERCLCPFGTQR 213
 Db 96 LLANFRNRLRSV-EALLGRALKQFFLGRPVSDFKRQAEPWLSSLRQGDGDDG 153
 Qy 214 QLAALQGSRVK---LLRRIAVFTLVSGAEDPLPYQCRDIAHDPGARFELIEGM 269
 Db 154 LLGAAVALGKLLWDLDSRALKDIKVPTLVWGTDDPLVLDASEKLSALIPNAEVVDDA 213
 Qy 270 GH---DIPERHIPRILEI 285
 Db 214 GHLLALEKPE-EVAELIKFL 232

RESULT 11
 US-10-289-148-4
 Query Match 13.1%; Score 198; DB 4; Length 232;
 Best Local Similarity 31.5%; Pred. No. 1.9e-11;
 Matches 82; Conservative 36; Mismatches 90; Indels 52; Gaps 12;

Qy 50 PRVICFDNRDAGLSTKLEGVKPKNIARYFLLASMGLKPRVPYPTIDDMALDTVGIMDALGI 109
 Db 1 FRYVLDLRFGESSPSD-----LAE-----YRFDLDAEDLEALLDALGL 40
 Qy 110 ESTHV-VGVSMGGMAQILGAKHGE-RVKSLTIMITSSGNPRM-----PRPVQLK 160
 Db 41 EKPVILVGHSMGGAAIAYAKYPELRYKALVLV-----SPPLPAGLSSDLFRQGNLEG 95
 Qy 161 FM-----RVPKSMDKEEWMKVNLLTITGSPGU-DREKLALDVRKSSTERCLCPFGTQR 213
 Db 96 LLANFRNRLRSV-EALLGRALKQFFLGRPVSDFKRQAEPWLSSLRQGDGDDG 153
 Qy 214 QLAALQGSRVK---LLRRIAVFTLVSGAEDPLPYQCRDIAHDPGARFELIEGM 269
 Db 154 LLGAAVALGKLLWDLDSRALKDIKVPTLVWGTDDPLVLDASEKLSALIPNAEVVDDA 213
 Qy 270 GH---DIPERHIPRILEI 285
 Db 214 GHLLALEKPE-EVAELIKFL 232

RESULT 11
 US-09-971-490-14
 Sequence 14, Application US/09971490
 GENERAL INFORMATION:
 - APPLICANT: Meyers, Rachel A.
 - CURTIS, Rory A. J.
 - APPLICANT: Bandaru, Rajasekhar
 - TITLE OF INVENTION: 48120, 23479 AND 46689, NOVEL HUMAN HYDROLASES
 - TITLE OF INVENTION: AND USES THEREOF
 - FILE REFERENCE: 10448-100001
 - CURRENT APPLICATION NUMBER: US/09/971,490
 - CURRENT FILING DATE: 2001-10-05
 - PRIOR APPLICATION NUMBER: 60/238,170
 - PRIOR FILING DATE: 2000-10-05
 - PRIOR APPLICATION NUMBER: 60/237,991
 - PRIOR FILING DATE: 2000-10-05
 - NUMBER OF SEQ ID NOS: 20
 - SOFTWARE: FastSEQ for Windows Version 4.0
 - LENGTH: 232
 - TYPE: PRT
 - ORGANISM: Artificial Sequence
 - FEATURE:
 - OTHER INFORMATION: Consensus sequence
 US-09-971-490-14

RESULT 13
US -10-038-854-66

Publication 66, Application US/100388854
Publication No. US20040022781A1

GENERAL INFORMATION:

APPLICANT: Spytek, Kimberly A
Liu, Li

APPLICANT: Woleinc, Adam R

APPLICANT: Vernet, Corine

APPLICANT: Eisen, Andrew J

APPLICANT: Liu, Xiaohong

APPLICANT: Malvankar, Uriel M

APPLICANT: Shinketsu, Richard A

Tchernov, Velizar

Spaderna, Steven K

Gorman, Linda

Kekuda, Ramesh

Patturajan, Meera

Gusev, Vladimir Y

Gangoli, Esha A

Guo, Xiaojia S

Shenoy, Suresh G

Rascelli, Luca

Casman, Stacie J

Boldog, Ferenc

Burgess, Catherine E

Edinger, Shlomit R

Elleman, Karen

Gunther, Erik

Smithson, Glenda

Millet, Isabelle

Macdougall, John R

FILE REFERENCE: 21402-230

CURRENT APPLICATION NUMBER: US/10/038,854

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: 60/258,928

PRIOR FILING DATE: 2000-12-29

PRIOR APPLICATION NUMBER: 60/259,415

PRIOR FILING DATE: 2001-01-02

PRIOR APPLICATION NUMBER: 60/259,785

PRIOR FILING DATE: 2001-01-04

PRIOR APPLICATION NUMBER: 60/269,814

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/279,832

PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/279,833

PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/286,683

PRIOR FILING DATE: 2001-04-25

NUMBER OF SEQ ID NOS: 411

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 66

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-10-038-854-66

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 411

SEQUENCE: 13 1% Score 198; DB 4; Length 232;

Best Local Similarity 31.5%; Pred. No. 1.9e-11;

Matches 82; Conservative 36; Mismatches 90; Indels 52; Gaps 12;

Software: PatentIn Ver. 2.1

Length: 232

Query Match

Best Local Similarity

Matches

Conservative

NUMBER OF SEQ ID NOS: 411

SEQUENCE: 13 1% Score 198; DB 4; Length 232;

Best Local Similarity 31.5%; Pred. No. 1.9e-11;

Matches 82; Conservative 36; Mismatches 90; Indels 52; Gaps 12;

Software: PatentIn Ver. 2.1

Length: 232

Db 1 FVILLDLRGFGESSPSD ----- LAE ----- YRFDDLAEDLEALLDALGL 40
QY 110 ESTHV-VCVSMGEMTAQILQAGAKHGE-RYKSLLTMITSGGNPRMPA-----'PRPVOLK 160
Db 41 EKPVILVGHSMGAAIALLYAAKYPELRYKALTVV-----SPPLPAGLSSDLPFRQGNDEG 95
QY 161 FM---- RPKSMDKEEWIKYNLELLTIGSCL-DREKLADLVRSKSTERCLCPETOR 213
Db 96 LLIJANFRURLSRV-ELALGRALKOFFLGRPLVSDLEKQADWLSSLIROGEDDGGS 153
QY 214 QLARIQSSSRVK---LLRITAVPTLVISGADDPLLYQCGRDIAHDIPARFELIBEM 269
Db 154 LIGRAVAKLQLWODLSALKDVKYUWGTDPVLVDASEKLSALIPNAEVVVIDA 213
QY 270 GH---DIPERHYPRLTELI 285
Db 214 GHLLALEKPE-EVAELIKFL 232

RESULT 14
US-10-193-452-36
Sequence 36, Application US/10193452
Publication No. US20040214758A1
GENERAL INFORMATION:
APPLICANT: Mayes, Rachel E
APPLICANT: Gluckemann, Maria Alexandra
APPLICANT: Curtis, Rory A. J.
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: NOVEL HUMAN HYDROLASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-194001
CURRENT APPLICATION NUMBER: US/10/193,452
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US 09/816,664
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,973
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 09/841,880
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199,559
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/862,556
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: PCT/US01/16424
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/206,036
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/861,165
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: PCT/US01/16014
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,442
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/875,353
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18335
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,949
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: US 09/896,578
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/20880
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/214,948
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/911,150
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: PCT/US01/23153
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220,008
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 09/911,317
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: PCT/US01/23160

PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220, 040
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 09/934, 323
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26091
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226, 774
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/963, 059
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: PCT/US01/29962
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/235, 033
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US 09/971, 490
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: PCT/US01/31674
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/238, 170
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 10/071, 275
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: PCT/US02/03793
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: US 60/267, 054
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: US 09/888, 911
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: PCT/US01/19967
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213, 688
PRIOR FILING DATE: 2000-06-23
SOFTWARE: Seq ID NOS: 104
SEQ ID NO: 36
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: consensus sequence
US-10-193-452-36

FEATURE:
Query Match 13.1%; Score 198; DB 4; Length 232;
Best Local Similarity 31.5%; Pred. No. 1.9e-11; Indels 52; Gaps 12;
Matches 82; Conservative 36; Mismatches 90;

Qy 50 FRVICEDNRDAGLSTKLEGIVKKPNIARVFLASMGKLPVPRPYTDDMALDTVGIMDALGI 109
Db 1 FRVILDLRGFGESSPDS-----LAE-----YRFDDLADEALLDALGI 40

Qy 110 ESTHY-VGVNGGMQAQILGAKHGE-RVSKTMLMTISSNPRMPA-----PREPVQLR 160
Db 41 EKPVLTVGHSMGGATAVAYAKYPLRVQLVLV----SPPDLAGLSSDLPFRQGNLG 95

Qy 161 FM-----RVPKSMKDKEEWIKYNULELLTIGSPGL-DREKLALDVRKSTERCLCPEGTOR 213
Db 96 LLLANFRNRLRSRV-EALLGRALQFFLGRPLVSDFRKQAEWMSSI.RQGDGGNG 153

Qy 214 QLAATLOSSRVK---LERRIAVTPLVSGAEDPLPVOCGRDIAHDHPGARFELIEGM 269
Db 154 LLGAAVALGKLUQWDLISALDIKVPTLWGTDDPLVDASEKLSALIPNAEVVDDA 213

Qy 270 GH---DIPPERHPIPLIELI 285
Db 214 GHLLALEKPE-EVAELIKFL 232

RESULT 15
US-10-193-452-87
Sequence 87, Applicant US/10193452
Public No. US20040214758A1
GENERAL INFORMATION: PCT/US02/03793

```

; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/267,054
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 09/888,911
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/US01/19967
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,688
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 87
LENGTH: 232
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-10-193-452-87

Query Match          13.1t;  Score 198;  DB 4;  Length 232;
Best Local Similarity   31.5t;  Pred. No. 1.9e-11;
Matches      82;  Conservative 36;  Mismatches 90;  Indels 52;  Gaps 12;
OQy
50 PRVICEDNRDAGLISLTCEGVKKPNIAVVELASMGKPFPRVPTLDMDALTYGLMDALGI 109
1 FRVILDLRGRGESSPSD-----LAE-----YRFDDIAEDLEALIDALGL 40
Dy
110 ESTHV--VGVSNSGMLAQILGAKHGB--RVKSLTLMITSNSGNPMPA-----PRPVQLQK 160
41 EKPVILVGHNSGGAAHLAYAKYPERVALVY----SPPLPGLOSSDLPFGQNLG 95
Db
161 FM-----RVPKSMDKEWIKYNLELLITTSGPL-----DREKLADVRKSIERCLCPEGTQR 213
96 LLANFRNRSRSV--BAILGRALKDFLLGRPLVSDFLKQAEWDWLSLIRQEDGDG 153
Dy
214 QLAIALQSRSVK---LLRRIAVPFLVISGEDPLPYQCBRDIAHIGARFELLEG 269
Db
154 LLGARVALGKQIOWDLSALKDIKVPTLVINGTDDPLVLDASEKSLALIPNAEVVVDDA 213
Dy
270 GH---DIPERHIPRIIELI 285
214 GHIAKFKPKEF-EVATIKFET 232

```

protein - protein search, using sw model	US-10-688-4900-2	Sequence 33303, A	
on:	April 13, 2006, 13:11:49 ;	Search time 27 Seconds (without alignments)	
		462.661 Million cell updates/sec	
file:	1509	Sequence 33302, A	
refl. score:	1 MAQVKANGITLBYEQGHRH.....ERHIPRLIELIAGHAAAEAA 294	Sequence 33301, A	
quence:		Sequence 4795, AP	
oring table:	BLOSUM62	Sequence 226, APP	
	Gapext 10.0 , Gapext 0.5	Sequence 10293, A	
217505. seqs,	42489236 residues	Sequence 5644, AP	
searched:		Sequence 30, APP1	
		Sequence 25602, A	
		Sequence 13018, A	
		Sequence 13017, A	
26	128	8.5	
	27	128	8.5
	28	128	8.5
	29	124	8.2
	30	122	8.1
	31	121.5	8.1
	32	120.5	8.0
	33	120.5	8.0
	34	119	7.9
	35	117.5	7.8
	36	117.5	7.8
	37	117	7.8
	38	117	7.8
	39	117	7.8
	40	114.5	7.6
	41	113	7.5
	42	113	7.5
	43	111.5	7.4
	44	110.5	7.3
	45	110.5	7.3
		Sequence 5989, AP	
		Sequence 5988, AP	
		Sequence 5987, AP	
		Sequence 6768, AP	
		Sequence 33701, A	
		Sequence 28, APP1	
		Sequence 6077, AP	
		Sequence 9507, AP	
		Sequence 21969, A	
260	7	US-11-096-568A-33303	
	273	7	
	282	7	
	267	7	
	331	6	
	302	7	
	311	6	
	334	6	
	293	7	
	487	7	
	546	7	
	284	7	
	401	7	
	416	7	
	311	7	
	324	7	
	380	6	
	259	7	
	7.3	US-11-087-099-6077	
	7.3	US-11-087-099-568A-21969	
	399	7	

Digitized by Google

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

-abase : Published Applications AA_New:
 1: /SDSS/prodata/1/pubaa/us08_new_pub_pep:
 2: /SDSS/prodata/1/pubaa/us06_new_pub_pep:
 3: /SDSS/prodata/1/pubaa/us07_new_pub_pep:
 4: /SDSS/prodata/1/pubaa/pct_new_pub_pep:
 5: /SDSS/prodata/1/pubaa/us03_new_pub_pep:
 6: /SDSS/prodata/1/pubaa/us10_new_pub_pep:
 7: /SDSS/prodata/1/pubaa/us11_new_pub_pep:
 8: /SDSS/prodata/1/pubaa/us60_new_pub_pep:
 RESULT 1
 US-11-087-099-1714
 ; Sequence 1714, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(5345)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NOS: 12464
 ; LENGTH: 260

סודות

APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo

TITLE OF INVENTION: GBN CLUSTER FOR RAMOPLANIN BIOSYNTHESIS

FILE REFERENCE: 3002-ZUS

CURRENT APPLICATION NUMBER: US/11/205,109

PRIOR APPLICATION NUMBER: US/09/976,059

PRIOR FILING DATE: 2001-10-15

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 46

SEQ ID NO: 10

LENGTH: 271

ORGANISM: Actinoplanes sp.

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (1) .(1)

OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that

the biosynthesized protein will have a formylmethionine residue

OTHER INFORMATION: at this position
US-11-205-109-10

Query Match Score 204; DB 7; Length 271;
Best Local Similarity 25.0%; Pred. No. 1.4e-11;

Matches 78; Conservative 38; Nsmatches 120; Indels 76; Gaps 9;

Qy 4 VKANGITLVEEOGRHHSMLLIMGLGGOLIDWPEEFIRGLAERGFRVICFDNRDA 63

Db 9 VTTNGTRLAVERSGAGE-PVLMINGSSAGQTWTWVHQPALHEAGYSTVFSDR--- 61

Qy 64 TKLEGVKPKNIAVPFLLASNLKPRVPTYDDMALTGIMDALGIESTHVGYSMGMI 123

Db 62 ---GPPSDV-----PAGKYSLADMTADTRGIEALDLPAPRIVGETSLGANI 105

Qy 124 AQILGAKKHGERVKSSTLMITSSGNPRMPAPRQ---VTKFMRVPKSNDK---- 170

Db 106 AQELAVDHPPEVCAVLIATLARPDAAQAQNQADIDJESGTULPAAYEAATAAVKMFES 165

Qy 171 -----EEWIKYNLELTIGSPGIDREKLADLVRSIERCLCPGTOROLAATIQ 220

Db 166 PATNDDVAREVLDI-FELSGTGYSAG-----GOAWELL- 199

Qy 221 SGSRVKKLIRRIAVPTLVISGAEDPLPYQCGRDIADHTPSARFELIEIGH---DIPER 276

Db 200 TGDRRAALRSVTPRVSISPADDLITPPHIAAEVAAIDCDLVEISRCHGLGYLERPDA 259

Qy 277 HIPRLIELIAGH 288

Db 260 VNAAALLEFDOSH 271

LENGTH: 224

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

RESULT 3

US-11-087-099-5676

sequence 5676, Application US/11087099

Publication No. US2000041361A1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REFERENCE: 38-21(53450)B EP

CURRENT APPLICATION NUMBER: US/11/087,099

CURRENT FILING DATE: 2005-03-22

NUMBER OF SEQ ID NOS: 12464

LENGTH: 312

TYPE: PRT

ORGANISM: Rhodobacter sphaeroides

US-11-087-099-5676

Query Match Score 201.5; DB 7; Length 312;

Best Local Similarity 24.4%; Pred. No. 3e-11;

Matches 71; Conservative 42; Nsmatches 105; Indels 73; Gaps 8;

Qy 1 MAQVANGITLVEEOGRHHSMLLIMGLGGOLIDWPEEFIRGLAERGFRVICFDNRDA 60

Db 51 MPHAEIGDURLNVLDDEGATGAPVFAHALGSDFRIVW-DNLPLPQLQRLVYDRLRGH 108

Qy 61 GLSTKLEGVKPKNIAVPFLLASNLKPRVPTYDDMALTGIMDALGIESTHVGYSMG 120

Db 109 GRST-----TPEPPYANGALIINDAERMEALSIREAVFGC5IG 147

Qy 121 GMIAQILGAKKHGERVKSSTLMITSSGNPRMPAPRQVQLQKFMRVPKSNDKBEWIK-YNLE 179

Db 148 GMIAQGLAVLKRLVGLVLCDTAA-----KIGTEPIW-----DRIDQVRSYGE 193

Qy 180 LUTTIGSPGLDREKLADLVRSIERCLCP-----EGTQROL-----AATIQ 220

Db 194 SLAD-----PTMKRWFAPAFRGPPEGQJWREFIPEGDPGYAGGAIA 237

Qy 221 SGSRVKKLIRRIAVPTLVISGAEDPLPYQCGRDIADHTPSARFELIEIGH 271

Db 238 GTDFYTTRTARLTLPALVGSEDGSTPDLVRETAELIERSREIVRGAGH 288

RESULT 4

US-11-054-281-303

; Sequence 303, Application US/11054281

; Publication No. US20060013813A1

; GENERAL INFORMATION:

; APPLICANT: Mezes et al.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-240CIP

; CURRENT APPLICATION NUMBER: US/11/054,281

; PRIOR APPLICATION NUMBER: 60/261,014

; PRIOR FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: 60/261,014

; PRIOR FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: 60/261,018

; PRIOR FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: 60/318,410

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/261,013

; PRIOR FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: 60/261,026

; PRIOR FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: 60/261,029

; PRIOR FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: 60/313,170

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 10,044,564

; PRIOR FILING DATE: 2002-01-11

; NUMBER OF SEQ ID NOS: 324

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 303

; LENGTH: 224

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:consensus

; OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-11-054-281-303

Query Match Score 12.8%; Score 193; DB 7; Length 224;

Best Local Similarity 28.1%; Pred. No. 1.2e-10;

Mismatches 71; Conservative 31; Gaps 9;

Indels 80;

Length 224;

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

Db 91 LLANFRNRLRSVEALLGRALKQFFLGRP-----LVSDLKQFE-----LS 133
 Qt 218 ILQSS-----SRVNL-----LRRZIAVPTLVISGAEDPLPYYQCERDIADI 258
 Db 134 LIRFGEDDDGGLWALGKLQLQDVSABLKRIKVPUVTLVWGGDDPLVPDASEKSLAFLA 193
 Qy 259 PGARFELIGGMGH 271
 Db .194 PNAEVVVIDDAGH 206

RESULT 5
 US-11-057-099-4437
 ; Sequence 4437, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-1(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; SEQ ID NO: 4437
 ; LENGTH: 265
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens str. C58 (Cereon)
 ; NUMBER OF SEQ ID NOS: 12464

Query Match 12.4%; Score 187; DB 7; Length 265;
 Best Local Similarity 28.0%; Pred. No. 5.6e-10;
 Matches 83; Conservative 36; Mismatches 89; Indels 88; Gaps 12;

Qy 22 PSMLIIMGQQLDWPEPIRGIAERGRVICPDNRDAGLSTKLEGYKPNITARVILLA 81
 Db 23 PVIAFINSGTDFRIW-DAVIEALGD-DYAYVLHDKRKGHLGSL----- 62
 Qy 82 SMGLKPRVPTYDLMALDTVGGLMDALGIESTHYGVSMGGMIAQILGAKHGERVKSLTLM 141
 Qy 63 DVG---RAYSIDPHAGDLALLDHLTEIKSIAVIGLSSVGLIAQGLYARRPDIVRALLLS 119
 Qy 142 ITSS--GNRMPAPRPQVQKEMRVPKSMDEKEWIKYNIELLTIGSPGDLREKLAIDVR 199
 Db 120 NTAIHRIGTEMNNAR-----IDK-----IAADG-----LASLVD 148
 Qy 200 KSFERCLCEPGTQRQLAAILQSGSRVKKR-----RIAVPTL 236
 Db 149 PWNERWFTPAFQRENAA-YAGARNMLSQQPEAGYSGTCAAIRDADFTEQAGRIVPAL 206

Query Match 12.4%; Score 187; DB 7; Length 265;
 Best Local Similarity 28.0%; Pred. No. 5.6e-10;
 Matches 83; Conservative 36; Mismatches 89; Indels 88; Gaps 12;

Qy 23 SMMLIIMGQQLDWPEPIRGIAERGRVICPDNRDAGLSTKLEGYKPNITARVILLA 82
 Db 15 TLVFIGSLGSSTDWMWFLQI-----DALHKDFERVIAVDRHGHSELIGT-PTVA----- 63
 Qy 83 MGUKPRVPTYDLMALDTVGGLMDALGIESTHYGVSMGGMIAQILGAKHGERVKSLTLM 142
 Db 64 -----DLAQDVLDLTDLGVGNFGTVGLGSAQVLAAT-SDRTKAAMC 110
 Qy 143 TSS--GNP----RMAPRPQ-----VLOKEMRVPKSMDEKEWIKYNIELLTIGSP 187
 Db 111 TAAGKGEFPQGMWLDRAACRENTGSSLSEAVIQRWPS-PTWLENNPASNEHFEAMVA-CTP 168
 Qy 188 GLDREKLAIDVRSKIEROLCPGQTOROLAATIQLQSGSVKLARRIAVPLVISAEDPLP 247
 Db 169 -----SEGVALCCCA-----LATWDFTDRGEITPVULTIAGDStP 207
 Qy 248 YQCGRDIAHDHIPS-ARPELIEGMGHDI PERIPH-----RLBLEIGHAA 290
 Db 208 PATVQITADGVCESAREVL-----PAAHVPTVERPNEVNLLOHFA 251

RESULT 7
 US-11-087-099-9057
 ; Sequence 9057, Application US/11087099
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; SEQ ID NO: 9057
 ; LENGTH: 265
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens
 ; NUMBER OF SEQ ID NOS: 12464

Query Match 12.1%; Score 183; DB 7; Length 265;
 Best Local Similarity 27.7%; Pred. No. 1.3e-09;
 Matches 36; Conservative 82; Mismatches 90; Indels 88; Gaps 12;

Qy 22 PSMLIIMGQQLDWPEPIRGIAERGRVICPDNRDAGLSTKLEGYKPNITARVILLA 81
 Db 23 PVIAFINSLGTDERIWI-DAVIEALGD-DYAVYLHDKRKGHLGSL----- 62

RESULT 8
 US-11-087-099-967
 ; Sequence 967, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; SEQ ID NO: 12464
 ; LENGTH: 266
 ; ORGANISM: Acinetobacter calcoaceticus
 US-11-087-099-967

Query Match 11.7%; Score 176.5; DB 7; Length 266;
 Best Local Similarity 24.7%; Pred. No. 5.Se-09;
 Matches 71; Conservative 45; Mismatches 110; Indels 61; Gaps 11;

Qy 8 GITLEYEEQGHRRHPSMLIMGLGQLIDWPERFIRGLAERGPFRVICFDNRDAGLSTKL 67
 Db 14 GKTLSVQINGPENAPAIVSNSLGTDHGMWQPQ-VAALKSQ-TRVTVTDTRGHGQSDVIE 71
 Qy 68 GVKKPNIARVELLASMGLKPRVPYTLDDMALDTVGMDALGIESTHVVGSMMGMAIQIL 127
 Db 72 NT-----TQNLDGEDVLDLDALNTEKAHFCGISMGLTALWL 109

Qy 128 GAKHGERVKSLLT-----MITSSG-NPMPMPAPRPOVLOKEMRPVKS--MDKEBWIYN 177
 Db 110 GIYQAAARPSITVANSAAKIWTEDGWNAABAEAVANGLAIDLVASTHTRWFSDFKDYKNDN 169

Qy 178 LELTTIGSPGLDREKLAIDVRKSIERC--LCPEGTORQLAAILOSGRVKLLRRIAVPT 235
 Db 170 L-----AQTIQSLADTPAQGYANACRALAKADYREK-LASISIPT 209

Qy 236 LVISGAEDPLLPYQCGRDADHPIGARFELLEGMDHIDPERHIFPLIE-LJAGHAA 291
 Db 210 LIAGSADPVTTIDGEFMQHQICNQFEVIDA-SHLSNIEQEPEKFI 255

RESULT 10
 US-10-467-657-6664
 ; Sequence 6664, Application US/10467657
 ; Publication No. US2010052605B1A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPICANT: FONTANA Maria Rita
 ; APPICANT: PIZZA Mariagrazia
 ; APPICANT: MASIGNANI Vega
 ; APPICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEAR ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIORITY APPLICATION NUMBER: GB-0103424.8
 ; PRIORITY FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO: 6664
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-6664

Query Match 11.2%; Score 168.5; DB 6; Length 293;
 Best Local Similarity 27.5%; Pred. No. 3.6e-05;
 Matches 64; Conservative 44; Mismatches 84; Indels 41; Gaps 11;

Qy 72 PNIA-RVFLASMSG-----LKPRPYTYLDDMADTVGLMDA-----LGIB-----110

Db 46 PDAAKTYLIHWGANHAFDDLMRPLPATWPSAVDLPGHGDAFPFAQPFDEAAADGIA 105

Qy 111 -----SPTHVGSMGCMIAQITGAKIGERVKSLTL-----MITSGNPR-MPAPRQVL 158
 Db 106 AQDTSADILGWSLGSQGVALYAAHDKVRSCLTASFARITADYDPEGLAAP---AL 162

Qy 159 QKFMRVPKSMDKBEWVYKNLELLTTCGSPGLDREKLAIDVRKSIERCPEGTQRQLAII 218
 Db 163 GRMVGART-DYAKHKQFLQ-LQHHTP--DAAEITGRILPDLRGTPQALQELDAA 218

Qy 219 LOSGSRVYKLLRRIAVPTLVISGAEDPLLPYQCGRDADHPIGARFELJEGMCH 271
 Db 219 ERAÐAR-HLLDKIDDVPLVLFEGKDAITPLRMGEYLHRHLKGSRVYMEKAH 270

RESULT 9
 US-11-087-099-8501
 ; Sequence 8501, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US/11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; SEQ ID NO: 12464
 ; LENGTH: 266
 ; TYPE: PRT

RESULT 13
US-11-096-568A-25601
; Sequence 25601, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-15922PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25601
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 13492535
US-11-096-568A-25601

Query Match 9.7%; Score 147; DB 7; Length 308;
Best Local Similarity 23.1%; Pred. No. 4.1e-06;
Matches 76; Conservative 52; Mismatches 123; Indels 78; Gaps 13

3 QVKANGITLEYYFOG--HRHHPSMLIMGLGGQLIDWPBEIFRGAERGFRVICDNRDA 60
8 QLEANGITMVAEAGGPVNASAPAVLFGFPELMWSRHQ--MGYLLARGYRCVAPDLRGY 66

61 GLSTKLEGVKKNNIARVFLASNGLKPKVP--YTLDMDMALDTVGLMDAIGIBSTHVVGVS 118
67 GGT--APPPTDAAHLPQVYVGHQ 105

119 MGGMIAQILQGKGERYKSLSMITSSNPRMPAPRPOVLTQKEMVRPKSMDEKEWTKYNELLT 168
; MRVPKSM 168

106 WGAIVSNNLCLRPDRVRL-VNLSVATMPRRGKVKP--LEYFRAAYGDEYYVCRFQEPG 162

169 DKREWTKYNELLTII-----GSPLGLDREKLALDVYRKSIERCLCPEGTQRQLAILQS 221
163 LEAFATPDLSKSPFTLTLRATGSANDLRKNOTYSKOMVLPPWLSBDDVSYLSVSK 222

222 --GSRVKKLR-----RIVAYPTLVISGAEDEPLPYOCGRDIADHHPGARF 263
223 TGFAGGJNYVRCLDNLWELMAPTGAKVQYPTKFVGI-----DGSBLAYHPGVKR 272

264 ELEBGMGHDIPERHIPIJELLAGHAAA 292
273 YIHKG-GF--KRDPVMLEEVVVIKGAGA 297

RESULT 14
US-11-096-568A-25600
; Sequence 25600, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO: 25600
LENGTH: 330
ORGANISM: Zea mays subsp. mayss
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(330)
OTHER INFORMATION: Ceres Seq. ID no. 13492534
US-11-096-568A-25600

Query Match 9.7%; Score 147; DB 7; Length 330;

Best Local Similarity 23.1%; Pred. No. 4.5e-06;
Matches 76; Conservative 52; Mismatches 123; Indels 78; Gaps 13;

Qy 3 QVKANGITLVEEQG--HRHHPSPMLIMGLGQLIDWPPEFIRGLAERFRVICFDNDA 60

Db 30 QLBANGITLVEAQGPVNNSAPAVLFVHGFPPELMYSWRHQ-MGYLAAQYRCVAPDRLGY 88

Qy 61 GLSTKLEGTKKPNTARVFLLASMGLKPRVYP-YTLLDDMADTVGLMDAIGESTHVVGVS 118

Db 89 GGT-----APPETTSVTVFHTYDIVALLDALHLPQFVWHD 127

Qy 119 MGGMAQIQLGAKHGERVKSITLMTTSSGNPRMPAPRQVTLQKF-----MRVPKS 168

Db 128 WGAIVSWNLCLLRPRVRAL-VNLSSVAFNPRLPRPVKPK-LEYFRAAYDEYYVCRFQEPG 184

Qy 169 DKEEMIKYNEBLUTI-----SGPGLREKLADVERKSIERCLCPBTQOROAAATLQS 221

Db 185 LEAFATFDIKSPTFTLALTIRATSSAMPLRKNOTYSKCMVLSWLSEEDVSLASTYK 244

Qy 222 ---GSRVKLLR-----RIVAPTLYVISGAEDPULLPYQCGRDIAHDHPIGARF 263

Db 245 TGFAGGVNTYRCLDNWEAMPAWTKAKVYQVPTKPIVG-----DGDLAYHHEGVKR 294

Qy 264 EIIIGMGHIDPERHPIPLLEIAGHAAA 292

Db 295 YIHKG-GF---KRDPVMLBEBVVVTKGAGA 319

RESULT 15

US-11-096-568A-29097

Sequence 29097, Application US/11096568A

Publication No. US2006046240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOs: 34471

SEQ ID NO: 29097

LENGTH: 264

TYPE: PRF

ORGANISM: Arabidopsis thaliana

FEATURE:
NAME/KEY: misc_feature

LOCATION: (1)-(264)

OTHER INFORMATION: Ceres Seq. ID no. 3659149

Query Match 9.6%; Score 145.5; DB 7; Length 264;

Best Local Similarity 25.2%; Pred. No. 4.5e-06;
Matches 69; Conservative 34; Mismatches 114; Indels 57; Gaps 9;

Qy 18 HRHHPSPMLIMGLGQLIDWPPEFIRGLAERGRVVICFDNRDAGLSTYLEGVKPNJARV 77

Db 10 NRSKPNLLILHGFGANAKWQYGEHLRAFTGR-FNVTYVBDLFFGLSSTS---PNRTES 64

Qy 78 FLLASMGKPRVVPYTDMDALDTVGLMDALGIESTHYVGWSMGGMAQILGAKHGERVKS 137
Db 65 F-----QARCLMRMLEARGYORMNIVGISTYGGFVG'SLAAGOPENVFK 107
Qy 138 LTLMITSSGNPRMPAPRQVLOKFKMRVPKSMDXEEWIKYNELLTIGSPGLDREKLALD 197
Db 108 LVTCCAG----VCLBEKDMDGLFVTP-----NLEFAFGILLIPQTP-EKLKEL 150
Qy 198 VRKSIER-----CLCPESTQ-ROLAILQSGSRVCKLRRIAVPTLVSG 240
Db 151 IRSEFVRPKIGVPSFELWDWMCTEFEERDILKSILKORRLSDPRIOKSLIIWG 210
Qy 241 AEDPLLPYQCGRDIAHDI-PGARFELIEGMGHDI 273
Db 211 EEDQIFPLELGTRKRGHESKEIVVIKKAGHVA 244

Search completed: April 13, 2006, 13:14:56
Job time : 28 secs